

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:43 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

Hello, this is the search that I requested earlier today. It has been approved for a rush.
 Thanks so much for your help,
 Amy Bowman

-----Original Message-----

From: Richter, Johann
Sent: Friday, December 02, 2005 9:39 AM
To: Bowman, Amy
Cc: STIC-Biotech/ChemLib
Subject: RE: sequence search-10/773,678

Approved.

Johann R. Richter, Ph.D., Esq.
 Supervisory Patent Examiner
 Biotechnology and Organic Chemistry
 Art Unit 1621
 571-272-0646

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DEC - 2 2005
STIC-BIOTECH/CHEM LIBRARY
(STIC)

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:08 AM
To: Richter, Johann
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:07 AM
To: Chan, Christina; Hutzell, Paula
Subject: FW: sequence search-10/773,678

12/05/05
JTH

Hello,
 My SPE, Drew Wang, thought I should ask for a rush search for this case. Am I contacting the appropriate person to request this?
 Thank you,
 Amy Bowman

Point of Contact
P. Sheppard

 Searcher: _____
 Searcher Phone: _____
 Date Searcher Picked up: _____
 Date completed: _____
 Searcher Prep Time: _____
 Online Time: _____

 Type of Search
 NA# _____ AA# _____
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure #: _____ Text: _____
 Inventor: _____ Litigation: _____

 Vendors and cost where applicable
 STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other (Specify): _____

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-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 8:54 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

I meant to mention that this case is about to be allowed, so I will need to include the interference database...

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 7:31 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/773,678

Hello,

I need a search of SEQ ID NO: 342 in application 10/773,678, length limited to 30 nucleobases.

Thank you,

Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Unclassified.
1 (bases 1 to 20)
Karras,J.G.
Antisense modulation of stat3 expression
Patent : US 6159694-A 19 12-DEC-2000;
Location/Qualifiers
1. .0
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Organism "unknown"
/mol_type="genomic DNA"

REFERENCE 1 (bases 1 to 20)
Karras,J.G.
Antisense oligonucleotide modulation of STAT3 expression
Patent: US 6727054-A 19 27-APR-2004;
Location/Qualifiers
1. .20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
| | | | | | | | | |
Db 7 GACTCTTGCAGGAA 20
| | | | | | | | | |

RESULT 3

BD272619 BD272619 20 bp DNA linear PAT 17-JUL-2003
LOCUS Antisense oligonucleotide modulation of STAT3 expression.
DEFINITION BD272619
ACCESSION BD272619
VERSION GI:32082387
KEYWORDS JP 2002541784-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
REFSEQUENCE other sequences; artificial sequences.
1 (bases 1 to 20)
Karras,J.G.
Antisense oligonucleotide modulation of STAT3 expression
Patent: JP 2002541784-A 19 10-DEC-2002;
JIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002541784-A/19
PD 10-DEC-2002
PF 06-APR-2000 JP 2000611544
PR 08-APR-1999 US 09/288461
PI JAMES G KARRAS
PC C12N15/09; A61K31/711; A61K48/00; A61P29/00; A61P35/00;
PC A61P37/02
PC A61P43/00; C12N5/06; C12N15/00; C12NS/00 CC Antisense
oligonucleotide
PH Key
FT Source
FT /organism="Artificial Sequence".
FEATURES source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;

Qy 4 TCTTGAGGAAGGGCT 20
| | | | | | | | | | | |
Db 9 TTTTCAGGAGAGGCT 25
| | | | | | | | | | | |

RESULT 6

AR205609 AR205609 28 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 13 from patent US 6369038.
DEFINITION AR205609
ACCESSION AR205609
VERSION AR205609.1
KEYWORDS GI:21503235
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 28)
Blumenfeld,M.; Brandys,P.; d'Auriol,L. and Vasseur,M.
Closed antisense and sense oligonucleotides and their applications
Patent: US 6369038-A 13 09-APR-2002;
Location/Qualifiers
1. .28
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

RESULT 4

AR531367 AR531367 20 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 19 from patent US 67227064.
DEFINITION AR531367
ACCESSION AR531367
VERSION AR531367.1
KEYWORDS GI:53919806
SOURCE Unknown.
ORGANISM Unknown.

Query Match 69.0%; Score 13.8; DB 6; Length 28;
Best Local Similarity 88.2%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
FEATURES Source Final Extension: 74 degrees C for 5.00 minutes.
LOCUS /organism="Canis familiaris"
DEFINITION /mol_type="genomic DNA"
ACCESSION /db_xref="taxon:9615"
VERSION /tissue_type="spleen"
KEYWORDS /dev_stage="adult"
SOURCE /tissue_lib="E. Ostrander, in pBluescript+"
ORGANISM /1..19
REFERENCE /primer_bind
AUTHORS /primer_bind
TITLE /primer_bind
JOURNAL /primer_bind
PATENT /primer_bind
PAT 03-JUL-2002
FEATURES /primer_bind
SOURCE /primer_bind
LOCATION/QUALIFIERS /primer_bind
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
ORIGIN /primer_bind
RESULT 9
LOCUS AX554614 /organism="synthetic construct"
DEFINITION Sequence 168 from Patent WO0246229.
ACCESSION AX554614
VERSION AX554614..1 GI:25898281
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimke,R.A., Spytek,K.A.,
Gill,J.E., Baumgartner,J.C., Mishra,V.,
Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0246229-A 168 13-JUN-2002;
FEATURES /organism="synthetic construct sequences."
SOURCE Curagen Corporation (US)
LOCATION/QUALIFIERS /1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer Sequence"
ORIGIN /primer_bind
RESULT 10
LOCUS AX703339 /organism="synthetic construct"
DEFINITION Sequence 568 from Patent WO02059313.
ACCESSION AX703339
VERSION AX703339..1 GI:29538385
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Li,L., Ballinger,R.A., Padigaru,M., Kakuda,R., Colman,S.D.,
Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Gusev,V.,
Malyanbar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J.,
Sciore,P., Macdougall,J.R., Gunther,E., Peyman,J.A., Ellerman,K.,
Gangolli,E.A. and Millet,I.
COMMENT G-protein coupled receptors and nucleic acids encoding same
JOURNAL Patent: WO 02059313-A 568 01-AUG-2002;

Query Match 69.0%; Score 13.8; DB 6; Length 28;
Best Local Similarity 88.2%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
FEATURES Source Final Extension: 74 degrees C for 5.00 minutes.
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DEFINITION /mol_type="genomic DNA"
ACCESSION /db_xref="taxon:9615"
VERSION /tissue_type="spleen"
KEYWORDS /dev_stage="adult"
SOURCE /tissue_lib="E. Ostrander, in pBluescript+"
ORGANISM /1..19
REFERENCE /primer_bind
AUTHORS /primer_bind
TITLE /primer_bind
JOURNAL /primer_bind
PATENT /primer_bind
PAT 27-NOV-2002
FEATURES /primer_bind
SOURCE /primer_bind
LOCATION/QUALIFIERS /primer_bind
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
ORIGIN /primer_bind
RESULT 9
LOCUS AX554614 /organism="synthetic construct"
DEFINITION Sequence 168 from Patent WO0246229.
ACCESSION AX554614
VERSION AX554614..1 GI:25898281
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimke,R.A., Spytek,K.A.,
Gill,J.E., Baumgartner,J.C., Mishra,V.,
Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0246229-A 168 13-JUN-2002;
FEATURES /organism="synthetic construct sequences."
SOURCE Curagen Corporation (US)
LOCATION/QUALIFIERS /1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer Sequence"
ORIGIN /primer_bind
RESULT 10
LOCUS AX703339 /organism="synthetic construct"
DEFINITION Sequence 568 from Patent WO02059313.
ACCESSION AX703339
VERSION AX703339..1 GI:29538385
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Li,L., Ballinger,R.A., Padigaru,M., Kakuda,R., Colman,S.D.,
Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Gusev,V.,
Malyanbar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J.,
Sciore,P., Macdougall,J.R., Gunther,E., Peyman,J.A., Ellerman,K.,
Gangolli,E.A. and Millet,I.
COMMENT G-protein coupled receptors and nucleic acids encoding same
JOURNAL Patent: WO 02059313-A 568 01-AUG-2002;

Query Match 67.0%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
FEATURES Source MAM 22-JAN-1996
LOCUS DOGP45501 /organism="synthetic construct"
DEFINITION Dog (Clone: CXX.455) primer for STS 455, 5' end.
ACCESSION L24340
VERSION L24340..1 GI:402053
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 1 of 2
SOURCE Canis Familiaris (dog)
ORGANISM Canis Familiaris
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;
Canis.
REFERENCE 8
AUTHORS Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
TITLE One hundred and one new simple sequence repeat-based markers for
the canine genome
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)
PUBLMED 7749226
COMMENT Original source text: Canis familiaris (library: E. Ostrander, in
pBluescript+) adult spleen DNA.
Submitted by:
Fred Hurchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia, Mailstop M318
Seattle, WA 98104, USA
e-mail: EOstrander@lbl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33

FEATURES	Curagen Corporation (US) Location/Qualifiers 1..26 /organism="synthetic construct" /mol type="unassigned DNA" /db_xref="taxon:37630" /note="PCR Primer Sequence"	VERSION AR359764.1 KEYWORDS Unknown. SOURCE Unknown. ORGANISM Unclassified.
ORIGIN	Query Match 65.0%; Score 13; DB 6; Length 26; Best Local Similarity 100.0%; Pred. No. 2.3e+05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; source	REFERENCE 1 (bases 1 to 20) AUTHORS Gatanaga,T. and Granger,G.A. TITLE Tumor necrosis factor receptor releasing enzyme JOURNAL Patent: US 6593456-A 134 15-JUL-2003; FEATURES Location/Qualifiers 1..20 /organism="unknown" /mol type="genomic DNA"
Qy	4 TCTTGAGGAAGC 16	ORIGIN
Db	3 TCTTGAGGAAGC 15	Query Match 64.0%; Score 12.8; DB 6; Best Local Similarity 87.5%; Pred. No. 2.9e+05; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 11	BD228539	Qy 4 TCTTGAGGAAGC 19 Db 1 TCTTGAGGAAGC 16
LOCUS	BD228539	RESULT 13
DEFINITION IL-17 homologous polypeptide and its application to remedy.	PAT 17-JUL-2003	A98434 LOCUS A98434 DEFINITION Sequence 18 from Patent WO912948. ACCESSION A98434 VERSION A98434..1 GI:6781535 KEYWORDS unclassified sequences. SOURCE unidentified ORGANISM unidentified
VERSION	BD228539..1 GI:31038309	REFERENCE 1 AUTHORS Landt,O. TITLE protein-coated polyribonucleic acids, method for the production thereof, and use of the same JOURNAL Patent: WO 912948-A 18 MAR-1999; FEATURES Location/Qualifiers 1..27 /organism="unidentified" /mol type="unassigned DNA" /db_xref="taxon:32644"
KEYWORDS	JP 2002515246-A/134.	ORIGIN
ORGANISM	unidentified	Query Match 64.0%; Score 12.8; DB 6; Best Local Similarity 87.5%; Pred. No. 2.9e+05; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
COMMENT	OS Unidentified PD 2002515246-A/134 PD 28-MAY-2002 PF 14-MAY-1999 JP 20000549734 PR 15-MAY-1998 US 60/085579, 23-DEC-1998 US 60/113621 PI UTIAN CHEN, ELEEN FILVAROFF, AUDLEY GODDARD, AUSTIN L GURNEY, PI HANZHONG LI, WILLIAM I WOOD PC C12N15/09, A61K38/21, A61K45/00, A61P19/00, C07K14/52, C07K16/24, PC C07K19/00, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/00 PC C12Q1/68, C12N15/00, PC A61K37/66, C12N5/00 CC Topology: Linear; Single; CC IL-17 homologous polypeptide and its application to remedy FH Key source 1..20 FT Location/Qualifiers Strandedness: Single; CC IL-17 homologous polypeptide and its application to remedy FH Key source 1..20 FT Location/Qualifiers Topology: Linear; CC IL-17 homologous polypeptide and its application to remedy FH Key source 1..20 FT Location/Qualifiers Strandedness: Single; CC IL-17 homologous polypeptide and its application to remedy FH Key source 1..20 FT Location/Qualifiers Topology: Linear; CC IL-17 homologous polypeptide and its application to remedy FH Key source 1..20 FT Location/Qualifiers Strandedness: Single;	
FEATURES	source	RESULT 14 AX576339 LOCUS AX576339 DEFINITION Sequence 14 from Patent EP1251138. ACCESSION AX576339 VERSION AX576339..1 GI:27646038 KEYWORDS synthetic construct SOURCE synthetic construct ORGANISM other sequences; artificial sequences. REFERENCE 1 AUTHORS Schaetzl,H. TITLE Prion protein dimers useful for vaccination JOURNAL Patent: EP 1251138-A 14 23-OCT-2002; FEATURES Location/Qualifiers
LOCUS	AR359764	Qy 4 TCTTGAGGAAGC 19 Db 1 TCTTGAGGAAGC 16
DEFINITION Sequence 134 from patent US 6593456.	PAT 17-AUG-2003	RESULT 12 AR359764 DEFINITION Sequence 134 from patent US 6593456. ACCESSION AR359764

source 1. .30
 /mol type="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer"

ORIGIN

Query Match, Score 12.6; DB 6; Length 21;
 Best Local Similarity 78.9%; Pred. No. 3.7e-05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCTTGAGGAAAGCGGC 19
 Db 10 TCCGTAAAGAAGCGGC 25

RESULT 17 AR361504
 LOCUS AR361504
 DEFINITION Sequence 30 from patent US 6599728.
 ACCESSION AR361504
 VERSION AR361504.1 GI:33769352

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Morin, G.B., Funk, W.D. and Biatyszek, M.A.
 TITLE Second mammalian tankyrase
 JOURNAL Patent: US 6599728-A 30-29-JUL-2003;
 FEATURES Location/Qualifiers 1. .21
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match, Score 12.6; DB 6; Length 21;
 Best Local Similarity 78.9%; Pred. No. 3.7e-05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTGAGGAAGCGCT 20
 Db 20 ACTCTGAAGGAAGATGCT 2

RESULT 18 AR081003
 LOCUS AR081003
 DEFINITION Sequence 86 from patent US 5969122.
 ACCESSION AR081003
 VERSION AR081003.1 GI:10007731

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Hammond, P.W. and Endoso, A.N.
 TITLE Nucleic acid hybridization assay probes, helper probes and
 amplification oligonucleotides targeted to mycoplasma pneumoniae
 JOURNAL Patent: US 5969122-A 86-19-OCT-1999;
 FEATURES Location/Qualifiers 1. .23
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match, Score 12.6; DB 6; Length 20;
 Best Local Similarity 78.9%; Pred. No. 3.7e-05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTGAGGAAGCGCT 20
 Db 20 AATCTCCAGGAAGCTGCT 2

RESULT 19 160352
 LOCUS C0B93797
 DEFINITION Sequence 85 from Patent WO2004087903.
 ACCESSION C0B93797
 VERSION C0B93797.1 GI:55166196

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE Liu, W., Wu, L., Channavajhala, P.L., Lin, L.L. and Zhang, Y.
 AUTHORS Novel protein homologous to kinase suppressor of ras
 TITLE Patent: WO 2004087903-A 85-14-OCT-2004;
 JOURNAL Wyeth (US)

FEATURES Location/Qualifiers 1. .21
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

LOCUS	J60352	Sequence 86 from patent US 5656427.	23 bp	DNA	linear	PAT 07-OCT-1997		Hominidae; Homo.
DEFINITION	J60352						REFERENCE	1
VERSION	J60352.1	GI:2478797					AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
SOURCE	Unknown.						TITLE	Myosin-like gene expressed in human heart and muscle
ORGANISM	Unknown.						JOURNAL	Patent: WO 0192524-A 13006 06-DEC-2001;
REFERENCE	1	(bases 1 to 23)					FEATURES	Location/Qualifiers
AUTHORS	Hammond,P.W. and Endozo,A.A.						Source	1..25 /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"
TITLE	Nucleic acid hybridization assay probes, helper probes and amplification oligonucleotides targeted to Mycoplasma pneumoniae nucleic acid						ORIGIN	
JOURNAL	Patent: US 5656427-A 86 12-AUG-1997;						Query Match	63.0%; Score 12.6; DB 6; Length 25;
FEATURES	Location/Qualifiers						Best Local Similarity	78.9%; Pred. No. 3.7e+05; Mismatches 4; Indels 0; Gaps 0;
source	1..23 /organism="unknown" /mol_type="unassigned DNA"						Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN							Qy	2 ACTCTTGAGGAAGGGCT 20
							Db	7 AGTCCTGCCAGAAGGGCT 25
Query Match	63.0%; Score 12.6; DB 6; Length 23;						RESULT 22	CQ628267
Best Local Similarity	78.9%; Pred. No. 3.7e+05; Mismatches 4; Indels 0; Gaps 0;						LOCUS	CQ628267
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						DEFINITION	Sequence 13007 from Patent WO0192524.
Qy	1 GACTTTGCGGAAACGGC 19						ACCESSION	CQ628267
Db	5 GACCTTAGGGCATGGC 23						KEYWORDS	CQ628267.1 GI:41678485
RESULT 20							SOURCE	Homo sapiens (human)
LOCUS	AX292865	Sequence 4627 from Patent WO0179548.	24 bp	DNA	linear	PAT 21-NOV-2001	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
DEFINITION	AX292865						REFERENCE	1
ACCESSION	AX292865						AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
VERSION	AX292865.1	GI:17054548					TITLE	Myosin-like gene expressed in human heart and muscle
KEYWORDS							JOURNAL	Patent: WO 0192524-A 13007 06-DEC-2001;
SOURCE							FEATURES	Location/Qualifiers
ORGANISM							Source	1..25 /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"
RESULT 20							ORIGIN	
LOCUS	AX292865/c	Sequence 4627 from Patent WO0179548.	24 bp	DNA	linear	PAT 21-NOV-2001	Query Match	63.0%; Score 12.6; DB 6; Length 25;
DEFINITION	AX292865						Best Local Similarity	78.9%; Pred. No. 3.7e+05; Mismatches 4; Indels 0; Gaps 0;
ACCESSION	AX292865						Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
VERSION	AX292865.1	GI:17054548					Qy	2 ACTCTTGAGGAAGGGCT 20
KEYWORDS							Db	6 AGTCCTGCCAGAAGGGCT 24
SOURCE							RESULT 23	CQ628268
ORGANISM							LOCUS	CQ628268
REFERENCE	1						DEFINITION	Sequence 13008 from Patent WO0192524.
AUTHORS	Gerry,N.P., Favis,R. and Kliman,R.						ACCESSION	CQ628268
TITLE	Method of addressing array for detection of nucleic acid sequence differences using ligase detection reaction						KEYWORDS	CQ628268.1 GI:41678486
JOURNAL	Patent: WO 0179518-A 4627 25-OCT-2001; CORNELL RESEARCH FOUNDATION, INC. (US)						SOURCE	Homo sapiens (human)
FEATURES	Location/Qualifiers						ORGANISM	Homo sapiens
source	1..24 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:2630" /note="Hypothetical Probe Sequence"						REFERENCE	1
ORIGIN							AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Query Match	63.0%; Score 12.6; DB 6; Length 24;						TITLE	Myosin-like gene expressed in human heart and muscle
Best Local Similarity	78.9%; Pred. No. 3.7e+05; Mismatches 4; Indels 0; Gaps 0;						JOURNAL	
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						FEATURES	
Qy	2 ACTCTTGCGGAAACGGCT 20						Source	
Db	23 ACTGTGCACTAACGGCT 5						ORIGIN	
RESULT 21							Query Match	63.0%; Score 12.6; DB 6; Length 25;
LOCUS	CQ628266	Sequence 13006 from Patent WO0192524.	25 bp	DNA	linear	PAT 02-FEB-2004	Best Local Similarity	78.9%; Pred. No. 3.7e+05; Mismatches 4; Indels 0; Gaps 0;
DEFINITION	CQ628266						Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	CQ628266						Qy	2 ACTCTTGAGGAAGGGCT 20
VERSION	CQ628266.1	GI:41678484					Db	6 AGTCCTGCCAGAAGGGCT 24
KEYWORDS							RESULT 23	CQ628268
SOURCE							LOCUS	CQ628268
ORGANISM							DEFINITION	Sequence 13008 from Patent WO0192524.
REFERENCE	1						ACCESSION	CQ628268
AUTHORS	Homo sapiens						KEYWORDS	CQ628268.1 GI:41678486
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.						SOURCE	Homo sapiens (human)

JOURNAL Patent: WO 0192524-A 13008 06-DEC-2001;
 Aeonica, Inc. (US)
 Location/Qualifiers
 1. .25

FEATURES source
 /mol type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match Score 12.6%; DB 6; Length 25;
 Best Local Similarity 78.9%; Pred. No. 3.7e-05;
 Matches 15; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCT 20
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 Db 5 AGTCCCTGCCAGAGGGCT 23

RESULT 24
 CQ628269 LOCUS CQ628269 Sequence 13009 from Patent WO0192524.
 DEFINITION DNA 25 bp linear PAT 02-FEB-2004
 ACCESSION CQ628269
 VERSION CQ628269..1 GI:41678487
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
 Shannon, M.E. Myosin-like gene expressed in human heart and muscle
 Patent: WO 0192524-A 13011 06-DEC-2001;
 Acomica, Inc. (US)

AUTHORS
 JOURNAL
 FEATURES
 1. .25
 /organism="Homo sapiens"
 /mol type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match Score 12.6%; DB 6; Length 25;
 Best Local Similarity 78.9%; Pred. No. 3.7e-05;
 Matches 15; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCT 20
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 Db 2 AGTCCCTGCCAGAGGGCT 20

RESULT 25
 CQ628270 LOCUS CQ628270 Sequence 13010 from Patent WO0192524.
 DEFINITION DNA 25 bp linear PAT 02-FEB-2004
 ACCESSION CQ628270
 VERSION CQ628270..1 GI:41678488
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
 Shannon, M.E. Myosin-like gene expressed in human heart and muscle
 Patent: WO 0192524-A 13012 06-DEC-2001;
 Acomica, Inc. (US)

AUTHORS
 JOURNAL
 FEATURES
 1. .25
 /organism="Homo sapiens"
 /mol type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match Score 12.6%; DB 6; Length 25;
 Best Local Similarity 78.9%; Pred. No. 3.7e-05;
 Matches 15; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCT 20
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 Db 4 AGTCCCTGCCAGAGGGCT 22

RESULT 26
 CQ628271 LOCUS CQ628271 Sequence 13011 from Patent WO0192524.
 DEFINITION DNA 25 bp linear PAT 02-FEB-2004
 ACCESSION CQ628271
 VERSION CQ628271..1 GI:41678489
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
 Shannon, M.E. Myosin-like gene expressed in human heart and muscle
 Patent: WO 0192524-A 13011 06-DEC-2001;
 Acomica, Inc. (US)

AUTHORS
 JOURNAL
 FEATURES
 1. .25
 /organism="Homo sapiens"
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ORIGIN

Query Match Score 12.6%; DB 6; Length 25;

Best Local Similarity 78.9%; Pred. No. 3.7e+05; Matches 15; Conservative 0; Nismatches 4;	Indels 0; Gaps 0;	RESULT 30	AR469331	25 bp DNA	linear	PAT 20-FBB-2004	
Qy 2 ACTCTTGAGGAAGGGCT 20	Db 1 AGTCCCTGCAAGGGCT 19	LOCUS	AR469331	Sequence 13008 from patent US 6686188.	DEFINITION	AR469331	
DEFINITION Sequence 13006 from patent US 6686188.	ACCESSION AR469329	ACCESSION AR469330	ACCESSION AR469331	ACCESSION AR469331	ACCESSION AR469331	ACCESSION AR469331	
VERSION AR469329.1	VERSION AR469330.1	VERSION AR469330.1	VERSION AR469331.1	VERSION AR469331.1	VERSION AR469331.1	VERSION AR469331.1	
KEYWORDS Unknown.	SOURCE Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	
REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	
JOURNAL Patent: US 6686188-A 13008 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13008 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13008 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13008 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	
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Query Match 63.0%; Score 12.6; DB 6; Length 25; Best Local Similarity 78.9%; Pred. No. 3.7e+05; Matches 15; Conservative 0; Nismatches 4;	Indels 0; Gaps 0;	RESULT 31	AR469332	25 bp DNA	linear	PAT 20-FBB-2004	
Qy 2 ACTCTTGAGGAAGGGCT 20	Db 7 AGTCCCTGCAAGGGCT 25	LOCUS	AR469332	Sequence 13009 from patent US 6686188.	DEFINITION	AR469332	
DEFINITION Sequence 13007 from patent US 6686188.	ACCESSION AR469330	ACCESSION AR469330	ACCESSION AR469331	ACCESSION AR469331	ACCESSION AR469331	ACCESSION AR469331	
VERSION AR469330.1	VERSION AR469330.1	VERSION AR469330.1	VERSION AR469331.1	VERSION AR469331.1	VERSION AR469331.1	VERSION AR469331.1	
KEYWORDS Unknown.	SOURCE Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	
REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	
JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	
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Query Match 63.0%; Score 12.6; DB 6; Length 25; Best Local Similarity 78.9%; Pred. No. 3.7e+05; Matches 15; Conservative 0; Nismatches 4;	Indels 0; Gaps 0;	RESULT 32	AR469333	25 bp DNA	linear	PAT 20-FBB-2004	
Qy 2 ACTCTTGAGGAAGGGCT 20	Db 6 AGTCCCTGCAAGGGCT 24	LOCUS	AR469333	Sequence 13010 from patent US 6686188.	DEFINITION	AR469333	
DEFINITION Sequence 13010 from patent US 6686188.	ACCESSION AR469330	ACCESSION AR469330	ACCESSION AR469331	ACCESSION AR469331	ACCESSION AR469331	ACCESSION AR469331	
VERSION AR469330.1	VERSION AR469330.1	VERSION AR469330.1	VERSION AR469331.1	VERSION AR469331.1	VERSION AR469331.1	VERSION AR469331.1	
KEYWORDS Unknown.	SOURCE Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	KEYWORDS Unknown.	
REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	REFERENCE 1 (bases 1 to 25)	
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.	
JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	FEATURES source	JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;	
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KEYWORDS	Unknown.	TITLE	Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle			
SOURCE	Unknown.	JOURNAL	Patent: US 6686188-A 13012 03 -FEB-2004;			
ORGANISM	Unclassified.	FEATURES	Amersham PLC; Buckinghamshire; GBX;			
REFERENCE	1 (bases 1 to 25)	SOURCE	Location/Qualifiers			
AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanze1,D.K., Rank,D.R., Chen,W. and Shannon,M.E.	DEFINITION	1 .25 /organism="unknown" /mol_type="genomic DNA"			
TITLE	Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle	ORIGIN				
JOURNAL	Patent: US 6686188-A 13010 03-FEB-2004;	Query Match	Score 12.6%; DB 6; Length 25;			
FEATURES	GBX;	Best Local Similarity	63.0%; Score 12.6%; DB 6; Length 25;			
SOURCE	Location/Qualifiers	Matches	78.9%; Pred. No. 3.7e+05; Mismatches 0; Indels 0; Gaps 0;			
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Best Local Similarity	78.9%; Pred. No. 3.7e+05; Mismatches 0; Indels 0; Gaps 0;	RESULT	35			
Matches	15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	LOCUS	BD133366/C			
Qy	2 ACTCTTGAGGAAGGGCT 20	DEFINITION	Amino acid sequence of antigen epitope recognized by anticancer human monoclonal antibody CLN-IgG and DNA nucleotide sequence encoding it.			
Db	3 AGTCTGCCAGAAGGGCT 21	ACCESSION	BD133366			
RESULT	33	VERSION	BD133366.1 GI:23228311			
AR469334	AR469334 Sequence 13011 from patent US 6686188.	KEYWORDS	JP 2000051785-A9.			
LOCUS	25 bp DNA	SOURCE	synthetic construct			
DEFINITION	AR469334	ORGANISM	synthetic construct			
ACCESSION	AR469334.1	REFERENCE	other sequences; artificial sequences. 1 (bases 1 to 26)			
VERSION	GI:42704391	AUTHORS	Hagiwara,H. and Aotsuka,Y.			
KEYWORDS	Unknown.	JOURNAL	Amino acid sequence of antigen epitope recognized by anticancer human monoclonal antibody CLN-IgG and DNA nucleotide sequence			
SOURCE	Unknown.	COMMENT	YOSHITIDE HIDEAKI HAGIWARA OS Artificial Sequence			
ORGANISM	Unclassified.	PN	PN JP 2002051785-A9			
VERSION	1 (bases 1 to 25)	PD	PD 19-FEB-2002			
KEYWORDS	Gu,Y., Ji,Y., Penn,S.G., Hanze1,D.K., Rank,D.R., Chen,W. and Shannon,M.E.	PF	PF 09-AUG-2000 JP 2000241927			
SOURCE	Unclassified.	PI	PI HIDEAKI HAGIWARA, YASUTUKI AOTSUKA			
ORGANISM	Gu,Y., Ji,Y., Penn,S.G., Hanze1,D.K., Rank,D.R., Chen,W. and Shannon,M.E.	PC	PC C12N15/09 C07K14/82//C12N1/21, C12R1:19, C12N15/00 CC To synthesize while referring to the sequence of human CC			
VERSION	1 .25 /organism="unknown" /mol_type="genomic DNA"	FEATURES	COMMENT vimentin Location/Qualifiers			
KEYWORDS	Unknown.	Qy	FH Key FT source FT /organism='Artificial Sequence'			
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ORGANISM	Unclassified.	ORIGIN	1 (bases 1 to 25)			
VERSION	1 (bases 1 to 25)	Query Match	Score 12.6%; DB 6; Length 26;			
KEYWORDS	Gu,Y., Ji,Y., Penn,S.G., Hanze1,D.K., Rank,D.R., Chen,W. and Shannon,M.E.	Best Local Similarity	63.0%; Score 12.6%; DB 6; Length 25;			
SOURCE	Unclassified.	Matches	78.9%; Pred. No. 3.7e+05; Mismatches 0; Indels 0; Gaps 0;			
ORGANISM	Unclassified.	Qy	1 GACTTTGCAAGAACGGCT 20 2 AGTCTGCCAGAAGGGCT 20			
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REFERENCE	1 (bases 1 to 25)	ACCESSION	AR172849			
AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanze1,D.K., Rank,D.R., Chen,W. and Shannon,M.E.	VERSION	AR172849			
		KEYWORDS	AR172849.1 GI:17912340			
		SOURCE	Unknown.			

medicines
JOURNAL Patent: WO 03004526-A 1175 16-JAN-2003;
FEATURES Molecular Engines Laboratories (FR)
Source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="rtaxon:9606"

ORIGIN

Query Match Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 TGCAGGGAGCGGCT 20
| ||||| |||||
Db 3 TCCAGGGAGCGGCT 16

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C	26 13 65.0	Aaf46590 IGFBP3 OI
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	28 13 65.0	Abp59220 Human G-P
	29 13 65.0	Abt04530 Human G-P
	30 13 65.0	Abt05715 GPCR rela
	31 13 65.0	Adh31280 Human G-P
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	33 12.8 64.0	Aci12520 Human mic
	34 12.8 64.0	Ach63464 DNA targ
	35 12.8 64.0	Ach51423 DNA targ
	36 12.8 64.0	Ach53400 DNA targ
	37 12.8 64.0	Aax2793 PCR prime
	38 12.8 64.0	Adc51654 S' PCR Pro
	39 12.8 64.0	Abz2123 Mouse fus
C	40 12.6 63.0	Adm92376 Pancreati
C	41 12.6 63.0	Adm14384 Human mPG
C	43 12.6 63.0	Adm14226 Human mPG
	44 12.6 63.0	Adp1993 Periodont
	45 12.6 63.0	Adr67642 Human ret
	45 12.6 63.0	AdS99577 Small intum
	45 12.6 63.0	AdS99577 Human ret

ALIGNMENTS

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 2: Geneseqn1990s; *
 3: Geneseqn2000s; *
 4: Geneseqn2001as; *
 5: Geneseqn2001bs; *
 6: Geneseqn2002as; *
 7: Geneseqn2002bs; *
 8: Geneseqn2003as; *
 9: Geneseqn2003bs; *
 10: Geneseqn.003cs; *
 11: Geneseqm2003ds; *
 12: Geneseqm2004as; *
 13: Geneseqm2004bs; *
 14: Geneseqm2005s; *

 RESULT 1
 1: ADZ11151
 2: ID ADZ11151 standard; DNA; 20 BP.
 3: XX
 4: AC ADZ11151;

 5: Human STAT3-specific antisense oligonucleotide - SEQ ID 342.
 6: XX
 7: DT 16-JUN-2005 (first entry)
 8: XX
 9: DE XX
 10: KW antisense oligonucleotide; antisense therapy; inflammation;
 11: KW antiinflammatory; rheumatoid arthritis; antirheumatic;
 12: KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
 13: KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma ; STAT3; 86;
 14: KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

 Homo sapiens.
 OS

SUMMARIES

result	No	Score	Query Match	Length	DB ID	Description
c	1	20	100.0	20	14	Adz11151 Human STA
c	2	20	100.0	29	14	Adz10957 Human STA
c	3	19	95.0	20	14	Adz10988 Human STA
c	4	19	95.0	20	14	Adz11150 Human STA
c	5	18	90.0	20	14	Adz11152 Human STA
c	6	17	85.0	20	14	Adz11149 Human STA
c	7	17	85.0	20	14	Adz11153 Human STA
c	8	16	80.0	20	14	Adw26449 EGFR inhib
c	9	15	75.0	20	14	Adz11154 Human STA
c	10	15	75.0	20	14	Adz11148 Human STA
c	11	14.4	72.0	29	2	Aar78506 Thiol-spe
c	12	14	70.0	20	3	Aac93168 Human STA
c	13	14	70.0	20	6	Aas96785 Human STA
c	14	14	70.0	20	14	Adz10828 Human STA
c	15	13.8	69.0	25	3	Aac96250 HLA DP1
c	16	13.8	69.0	28	2	Aac31029 Circular
c	17	13.6	68.0	20	12	Adm14825 Human mPG
c	18	13.6	68.0	30	13	Adr45889 PCR prime
c	19	13.6	68.0	30	13	Adr45885 PCR prime

CC nucleic acid molecules encoding human signal transducers and activators of transcription 3 (STAT3). The antisense oligonucleotides of the invention inhibit expression of human STAT3. The antisense oligonucleotides of the invention are useful for treating and preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g. breast, prostate, head and neck, brain, myelomas, melanomas, leukemias, and lymphomas). The present DNA sequence represents a human STAT3-specific antisense oligonucleotide. NOTE: The present sequence has a phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGGGCT 20
Db 1 GACTCTTGAGGAAGGGCT 20

RESULT 2
ADZ10967/c
ID ADZ10967 standard; DNA; 29 BP.
XX AC ADZ10967;
XX DT 16-JUN-2005 (first entry)
XX DE Human STAT3-specific nucleotide probe - SEQ ID 158.
XX DE Human STAT3-specific nucleotide probe - SEQ ID 158.
XX PT antisense oligonucleotide; antisense therapy; inflammation;
antinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3;
probe; ss.
XX OS Homo sapiens.
XX PA (KARR /) KARRAS J G.
XX PN US2005074879-A1.
XX PI Karras JG;
XX PD 07-APR-2005.
XX PF 06-FEB-2004; 2004US-00773678.
XX PR 06-APR-2000; 2000WO-US009054.
XX PR 11-JAN-2001; 2001US-00758881.
XX PR 14-NOV-2003; 2003US-00713139.
XX PS Example 18; SEQ ID NO 179; 149pp; English.

XX CC The invention comprises antisense oligonucleotides that are targeted to nucleic acid molecules encoding human signal transducers and activators of transcription 3 (STAT3). The antisense oligonucleotides of the invention inhibit expression of human STAT3. The antisense oligonucleotides of the invention are useful for treating and preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g. breast, prostate, head and neck, brain, myelomas, melanomas, leukemias, and lymphomas). The present DNA sequence represents a human STAT3-specific antisense oligonucleotide. NOTE: The present sequence has a phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

XX SQ Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX DR 2005-272408/28.

XX PT New antisense compound, useful for treating or preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head and neck, and brain cancer, myelomas, melanomas, leukemias, and lymphomas).
XX PR 06-APR-2000; 2000WO-US009054.
XX PR 11-JAN-2001; 2001US-00758881.
XX PR 14-NOV-2003; 2003US-00713139.
XX PA (KARR /) KARRAS J G.

XX PI Karras JG;
XX DR 2005-272408/28.
XX PT New antisense compound, useful for treating or preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head and neck, and brain cancer, myelomas, melanomas, leukemias, and lymphomas).
XX PR 06-APR-2000; 2000WO-US009054.
XX PR 11-JAN-2001; 2001US-00758881.
XX PR 14-NOV-2003; 2003US-00713139.
XX PA (KARR /) KARRAS J G.

XX The invention comprises antisense oligonucleotides that are targeted to nucleic acid molecules encoding human signal transducers and activators of transcription 3 (STAT3). The antisense oligonucleotides of the invention inhibit expression of human STAT3. The antisense oligonucleotides of the invention are useful for treating and preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g. breast, prostate, head and neck, brain, myelomas, melanomas, leukemias, and lymphomas). The present DNA sequence represents a human STAT3-specific probe.

XX SQ Sequence 29 BP; 8 A; 8 C; 7 G; 6 T; 0 U; 0 Other;
XX CC nucleic acid molecules encoding human signal transducers and activators of transcription 3 (STAT3). The antisense oligonucleotides of the invention inhibit expression of human STAT3. The antisense oligonucleotides of the invention are useful for treating and preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g. breast, prostate, head and neck, brain, myelomas, melanomas, leukemias, and lymphomas). The present DNA sequence represents a human STAT3-specific probe.

Query Match 100.0%; Score 20; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.5; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGAGGAAGGGCT 20
Db 26 GACTCTTGAGGAAGGGCT 7

RESULT 3

ADZ10988

ID ADZ10988 standard; DNA; 20 BP.

XX AC ADZ10988;

XX DT 16-JUN-2005 (first entry)

XX DE Human STAT3-specific antisense oligonucleotide - SEQ ID 179.

XX KW antisense oligonucleotide; antisense therapy; inflammation;
antinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3;
KW phosphorothioate; 2'-MOE wing.

XX OS Homo sapiens.

XX PN US2005074879-A1.

XX PD 07-APR-2005.

XX PF 06-FEB-2004; 2004US-00773678.

XX PR 06-APR-2000; 2000WO-US009054.

XX PR 11-JAN-2001; 2001US-00758881.

XX PR 14-NOV-2003; 2003US-00713139.

XX PA (KARR /) KARRAS J G.

XX XX

XX PN US2005074879-A1.

XX PI Karras JG;

XX DR 2005-272408/28.

XX PT New antisense compound, useful for treating or preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head and neck, and brain cancer, myelomas, melanomas, leukemias, and lymphomas).

XX PT

XX PR 11-JAN-2001; 2001US-00758881.

XX PR 14-NOV-2003; 2003US-00713139.

XX XX

XX PS Example 18; SEQ ID NO 179; 149pp; English.

XX XX

XX CC

CC The invention comprises antisense oligonucleotides that are targeted to nucleic acid molecules encoding human signal transducers and activators of transcription 3 (STAT3). The antisense oligonucleotides of the invention inhibit expression of human STAT3. The antisense oligonucleotides of the invention are useful for treating and preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g. breast, prostate, head and neck, brain, myelomas, melanomas, leukemias, and lymphomas). The present DNA sequence represents a human STAT3-specific antisense oligonucleotide. NOTE: The present sequence has a phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

XX SQ Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

XX DR 2005-272408/28.

XX PT

XX PR

Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 23; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGGGCT 19

Db 2 GACTCTTGAGGAAGGGCT 20

CC level of one or more prognostic RNA transcripts or their expression
 CC products in a biological sample comprising cancer cells obtained from the
 CC patient. The method of the invention is useful for predicting whether a
 CC patient is likely to respond well to treatment with an EGFR inhibitor,
 CC especially patients having: ovarian cancer, colon cancer, pancreatic
 CC cancer, non-small cell lung cancer, breast cancer, and head/neck cancer.
 CC The present DNA sequence represents a PCR primer which is specific for a
 CC prognostic marker of the invention.

SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.5e-02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAAGGGCT 20
 Db 1 CTTGCAGGAAGGGCT 16

RESULT 9

ADZ11154

ID ADZ11154

standard; DNA; 20 BP.

XX

AC ADZ11154;

XX

DT 16-JUN-2005 (first entry)

XX

DE Human STAT3-specific antisense oligonucleotide - SEQ ID 345.

XX

ID ADZ11154

standard; DNA; 20 BP.

XX

KW antisense oligonucleotide; antisense therapy; inflammation;

KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;

KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;

KW brain tumor; multiple myeloma; leukemia; lymphoma; STAT3; ss;

KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

OS Homo sapiens.

XX

DT 16-JUN-2005 (first entry)

XX

DE Human STAT3-specific antisense oligonucleotide - SEQ ID 345.

XX

ID ADZ11154

standard; DNA; 20 BP.

XX

KW antisense oligonucleotide; antisense therapy; inflammation;

KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;

KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;

KW brain tumor; multiple myeloma; leukemia; lymphoma; STAT3; ss;

KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

OS Homo sapiens.

XX

PS US2005074879-A1.

XX

PI KARRAS J G;

XX

PD 07-APR-2005.

XX

PR 06-FEB-2004; 2004US-00773678.

XX

PR 06-APR-2000; 2000WO-US009054.

XX

PR 11-JAN-2001; 2001US-00759881.

XX

PR 14-NOV-2003; 2003US-00713139.

XX

PA (KARR/) KARRAS J G.

XX

PS Example 19; SEQ ID NO 339; 149PP; English.

XX

PI KARRAS J G;

XX

WPI 2005-272408/28.

XX

PR 06-FEB-2004; 2004US-00773678.

XX

PR 06-APR-2000; 2000WO-US009054.

XX

PR 11-JAN-2001; 2001US-00759881.

XX

PR 14-NOV-2003; 2003US-00713139.

XX

PA (KARR/) KARRAS J G.

XX

PS Example 19; SEQ ID NO 345; 149PP; English.

CC The invention comprises antisense oligonucleotides that are targeted to
 CC nucleic acid molecules encoding human signal transducers and activators
 CC of transcription 3 (STAT3). The antisense oligonucleotides of the
 CC invention inhibit expression of human STAT3. The antisense
 CC oligonucleotides of the invention are useful for treating and preventing
 CC inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
 CC breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
 CC and lymphomas). The present DNA sequence represents a human STAT3-
 CC specific antisense oligonucleotide. NOTE: The present sequence has a
 CC phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 14; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAG 15
 Db 6 GACTCTTGCAGGAAG 20

RESULT 10

ADZ11148

ID ADZ11148

standard; DNA; 20 BP.

XX

AC ADZ11148;

XX

DT 16-JUN-2005 (first entry)

XX

DE Human STAT3-specific antisense oligonucleotide - SEQ ID 339.

XX

ID ADZ11148

standard; DNA; 20 BP.

XX

KW antisense oligonucleotide; antisense therapy; inflammation;

KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;

KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;

KW brain tumor; multiple myeloma; leukemia; lymphoma; STAT3; ss;

KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

OS Homo sapiens.

XX

PS US2005074879-A1.

XX

PI KARRAS J G;

XX

PR 07-APR-2005.

XX

DR 2005-272408/28.

XX

PT New antisense compound, useful for treating or preventing inflammatory

PT diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head

PT and neck, and brain cancer, myelomas, melanomas, leukemias, and

PT lymphomas). The present DNA sequence represents a human STAT3-

PT specific antisense oligonucleotide. NOTE: The present sequence has a

XX

PS Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

XX

Query Match 75.0%; Score 15; DB 14; Length 20;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCGGAAAGGGCT 20

Db 1 TTGCGGAAAGGGCT 15

XX Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX Claim 14; Page 48; 66pp; English.

XX The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular.

XX Sequence 25 BP; 4 A; 2 C; 6 G; 13 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 4 TCTTGAGGAGGGGT 20
9 TTTCGAGGAGGGCT 25

RESULT 16
ID AAQ31029 standard; RNA; 28 BP.
XX AAQ31029;
XX DT 25-MAR-2003 (revised)
DT 23-MAR-1993 (first entry)
DE Circular antisense oligonucleotide GT to inhibit HSV-1.
XX closed oligonucleotide; immunomodulation; antiviral; antitumour;
KW exonuclease resistant; Herpes Simplex virus; cyclic; ss.
OS Synthetic.
XX Key
FH Location/Qualifiers
FT misc_feature 1 /*tag= a
FT /note= "forms phosphodiester bond with 3'-OH of C at
FT position 28"
FT misc_feature
FT /*tag= b
FT /note= "forms phosphodiester bond with 5'-Phosphate group
FT of G at position 1"
XX WO9219732-A1.
XX 12-NOV-1992.
XX PF 24-APR-1992; 92WO-FR000370.
XX PR 25-APR-1991; 91FR-00005114.
XX PA (GEST) GENSET.
XX Blumenfeld M, Brandys P, Dauriol L, Vasseur M;
XX WPI; 1992-398859/48.

PT Cyclic sense or anti-sense closed oligo nucleotide(s) - useful for
PT therapeutic antiviral or anticancer agent, labelled diagnostic or
PT cosmetic applications, and natural immunomodulatory interteron inducer.
XX Example 6; Page 50; 85pp; French.
XX DR 08-APR-2004.

CC This is an example of a cyclic oligonucleotide of the invention. The
CC closed oligonucleotides are more resistant to exonuclease attack than
CC their linear counterparts. The nucleotides at position 1 and 28 are
CC brought into proximity for ligation by hybridisation to a complementary
CC linear oligonucleotide. The circularised form of oligonucleotide GT
CC inhibits HSV-1 multiplication (30% inhibition at 2μM and 65%
CC inhibition at 5μM). At these low concentrations, the circular
CC oligonucleotide has a higher inhibitory effect than its linear
CC counterpart. See AAQ31019-Q31028 for other examples. (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
SQ Sequence 28 BP; 3 A; 8 C; 12 G; 5 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 2; Length 28;
Best Local Similarity 88.2%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 3 CTCCTGCAGGAAGGGC 19
12 CTCCCTGCAGGAAGGGC 28

RESULT 17
ID ADM14825_c
ID ADM14825 standard; DNA; 20 BP.
XX XX
AC AC ADM14825;
XX DT 01-JUL-2004 (first entry)
XX DB Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1012.
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cyclooxygenase;
KW immunomodulator; cardiotonic; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
XX Homo sapiens.
OS synthetic.
XX Key
FH Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 1..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
PN 08-APR-2004.
PD 25-SEP-2003; 2003WO-US030374.
XX PR 25-SEP-2002; 2002US-0413549P.
PA (PHARMACIA CORP.
PI Giere JK;
XX WPI; 2004-305094/28.

XX New antisense compound, having a sequence targeted to a nucleic acid e.g.,
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.

XX Claim 4; SEQ ID NO 1012; 132pp; English.

CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1 which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissue; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antiidiabetic, immunomodulator, cardiotonic, neuroprotective,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ Query Match 68.0%; Score 13.6%; DB 12; Length 20;
Best Local Similarity 80.0%; Pred. No. 9.7e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 4; Gaps 0;

XX Query Match 68.0%; Score 13.6%; DB 12; Length 20;
ID ADR45885 standard; DNA; 30 BP.
AC ADR45885;
DB 18-NOV-2004 (first entry)

XX RESULT 19
ID ADR45885

XX AC ADR45885;

XX DB 18-NOV-2004 (first entry)

XX OS Synthetic.

XX PN WO2004071462-A2.

XX PD 26-AUG-2004.

XX PR 12-FEB-2004; 2004WO-US004518.

XX PR 12-FEB-2003; 2003US-0446909P.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PA (FUNC-) FUNCTIONAL GENETICS INC.

XX PI Yu X, Liu B, Li L;

XX DR WPI; 2004-615918/59.

XX PS Example; SEQ ID NO 6; 71PP; English.

CC The specification describes a method for reducing viral budding and

CC infectivity from a mammalian cell infected by an enveloped virus. The

CC method comprises contacting the mammalian cell with an agent that

CC modulates the interaction between a VPS28 protein and a TSG101 protein or

XX protein.
XX Example; SEQ ID NO 10; 71PP; English.
XX
PT The specification describes a method for reducing viral budding and
CC infectivity from a mammalian cell infected by an enveloped virus. The
CC method comprises contacting the mammalian cell with an agent that
CC modulates the interaction between a VPS28 protein and a TSG101 protein or
CC a VPS28 protein. The enveloped virus is selected from human
CC immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
CC virus. The agent especially comprises a small interfering RNA (siRNA)
CC targeting the VPS28 gene. The method of the invention is useful for
CC treating viral infections, including HIV infections. It may also be used
CC for evaluating and screening drugs that can be used for treating viral
CC infections. PCR primers ADR45888-ADR4589 were used to amplify a VPS28
CC mutant. The amplified product was used to produce vectors for use in the
CC method of the invention.
XX Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
SQ Query Match 68.0%; Score 13.6%; DB 13; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GACTCTTGCGAGGAAGGGCT 20
Db 8 GAGGCATGCGAGGAAGGGTT 27

XX RESULT 19
ID ADR45885
AC ADR45885;
DB 18-NOV-2004 (first entry)
XX DB PCR primer used to amplify a human VPS28-Flag fusion.
XX KW viral budding; viral infectivity; enveloped virus; VPS28 protein;
KW TSG101 protein; human immunodeficiency virus; HIV-1; HIV-II;
KW Marburg virus; Ebola virus; small interfering RNA; siRNA;
KW viral infection; HIV infection; PCR; primer; 86.
XX OS Synthetic.
XX PN WO2004071462-A2.
XX PD 26-AUG-2004.
XX PR 12-FEB-2004; 2004WO-US004518.
XX PR 12-FEB-2003; 2003US-0446909P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PA (FUNC-) FUNCTIONAL GENETICS INC.

XX PI Yu X, Liu B, Li L;
XX DR WPI; 2004-615918/59.
XX PS Reducing viral budding and infectivity from a human cell infected by an
PT enveloped virus (e.g. HIV) comprises contacting the cell with an agent
PT that modulates the interaction between a VPS28 protein and a TSG101
PT protein.
XX PS Example; SEQ ID NO 6; 71PP; English.
CC The specification describes a method for reducing viral budding and
CC infectivity from a mammalian cell infected by an enveloped virus. The
CC method comprises contacting the mammalian cell with an agent that
CC modulates the interaction between a VPS28 protein and a TSG101 protein or

CC that regulates the expression of a VPS28 gene, or an antibody that binds
 CC a VPS28 protein. The enveloped virus is selected from human
 CC immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
 CC virus. The agent especially comprises a small interfering RNA (siRNA)
 CC targeting the VPS28 Gene. The method of the invention is useful for
 CC treating viral infections, including HIV infections. It may also be used
 CC for evaluating and screening drugs that can be used for treating viral
 CC infections. PCR primers ADR45884-ADR45885 were used to amplify a VPS28-
 CC Flag fusion construct. The amplified product was used to produce vectors
 CC for use in the method of the invention.

XX Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;

SQ 68.0%; Score 13.6; DB 13; Length 30;

Best Local Similarity 80.0%; Pred. No. 1e+04; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 GACTCTTGAGGAAGCGGCT 20

8 GAGGCATGAGGAAGCGGTT 27

RESULT 21

ID ABQ03332 standard; DNA; 24 BP.
 XX ABQ03332;

Db 1 GACTCTTGAGGAAGCGGCT 20

8 GAGGCATGAGGAAGCGGTT 27

RESULT 22

ID ADR45887 standard; DNA; 30 BP.
 XX ADR45887;

AC ADR45887;
 XX DT 18-NOV-2004 (first entry)

DE PCR primer used to amplify the VPS28 mutant Vps28deltaN1.

XX viral budding; viral infectivity; enveloped virus; VPS28 protein;

KW TSG101 protein; human immunodeficiency virus; HIV-1; HIV-II;

KW Marburg virus; Ebola virus; small interfering RNA; siRNA;

KW viral infection; HIV infection; PCR; primer; ss.

XX Synthetic.

OS WO2004071462-A2.

PN WO2004071462-A2.

XX DR 2002-292068/33.

PD 26-AUG-2004.

XX PF 12-FEB-2004; 2004WO-US004518.

PR 12-FEB-2003; 2003US-0446909P.

PA (UYJO) UNIV JOHNS HOPKINS.

PA (FUNC-) FUNCTIONAL GENETICS INC.

XX Yu X, Liu B, Li L;

XX WPI; 2004-615918/59.

XX Reducing viral budding and infectivity from a human cell infected by an
 PT enveloped virus (e.g. HIV) comprises contacting the cell with an agent
 PT that modulates the interaction between a VPS28 protein and a TSG101
 PT protein.

XX Example; SEQ ID NO 8; 71pp; English.

XX The specification describes a method for reducing viral budding and
 CC infectivity from a mammalian cell infected by an enveloped virus. The
 CC method comprises contacting the mammalian cell with an agent that
 CC modulates the interaction between a VPS28 protein and a TSG101 protein or
 CC that regulates the expression of a VPS28 gene, or an antibody that binds
 CC a VPS28 protein. The enveloped virus is selected from human
 CC immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
 CC virus. The agent especially comprises a small interfering RNA (siRNA)
 CC targeting the VPS28 gene. The method of the invention is useful for
 CC treating viral infections, including HIV infections. It may also be used
 CC for evaluating and screening drugs that can be used for treating viral
 CC infections. PCR primers ADR45886-ADR45887 were used to amplify a VPS28

CC mutant. The amplified product was used to produce vectors for use in the
 CC method of the invention.

XX Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;

SQ 68.0%; Score 13.6; DB 13; Length 30;

Best Local Similarity 80.0%; Pred. No. 1e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGCT 20

Db 8 GAGGCATGAGGAAGCGGTT 27

RESULT 23

ID ABQ03332 standard; DNA; 24 BP.
 XX ABQ03332;

Db 1 GACTCTTGAGGAAGCGGCT 20

8 GAGGCATGAGGAAGCGGTT 27

RESULT 24

ID ABQ03332 standard; DNA; 24 BP.
 XX ABQ03332;

Db 1 GACTCTTGAGGAAGCGGCT 20

8 GAGGCATGAGGAAGCGGTT 27

Qy 6 TTGGAGGAGCGGCT 20

6 TGCGAGGAGCGGCT 20

XX Result 22
 ID AAZ89440 standard; DNA; 23 BP.

XX	US200323341-A1.	PN	US200323341-A1.
AC		XX	
XX	15-JUN-2000 (first entry)	XX	
DT		PD	18-DEC-2003.
XX	Human type IV collagen alpha-3 chain primer #40.	XX	
DB		PF	12-JUN-2002; 2002US-00170332.
XX		XX	
KW	Human; primer; immunogenic; alpha-3 chain; type IV collagen; therapy;	PR	12-JUN-2002; 2002US-00170332.
KW	autoantibody; Goodpasture's syndrome; immunosuppression; ss.	XX	
XX		PA	(CASEY W M.
OS	Homo sapiens.	PA	(CHEN/ COLTON H M.
XX	WO200011475-A1.	PA	(COLT/ CHEN J.
PN		PA	(TAYLOR/ TAYLOR J D.
XX		PA	(WEINER/ WEINER M P.
PD	02-MAR-2000.	XX	
XX		PI	Casey WM, Chen J, Colton HM, Taylor JD, Weiner MP;
PP	20-AUG-1999; 99WO-SB001416.	XX	
XX		DR	WPI; 2004-052156/05.
PR	21-AUG-1998; 98SE-00002788.	XX	
XX		PT	Detecting single nucleotide polymorphisms in target nucleic acids, useful
PA	(WIES-) WIESLAB AB.	PT	for e.g., in genotyping or in pathogen detection and identification,
XX		PT	comprises detecting the labels in the hybridization products.
PI	Wieslander J, Hellmark T;	XX	
XX		PS	Claim 1; SEQ ID NO 124; 60pp; English.
DR	WPI; 2000-246583/21.	XX	
XX		CC	The invention relates to a method of detecting a result from an
PT	Novel immunogenic region recognized by autoantibodies from goodpasture's	CC	identification reaction to identify a selected nucleotide in a target
PT	patients for detecting their presence in circulating body fluid comprises	CC	nucleic acid comprising detecting the label of the labelled detection
PT	a non-collagenous approximately a3 chain domain of type IV collagen.	CC	product in the hybridization products, the presence of the label
XX		CC	indicating the identity of the selected nucleotide in the target nucleic
PS	Example; Page 13; 30pp; English.	CC	acid. The method is useful for rapid detection of single nucleotide
XX		CC	polymorphisms in a nucleic acid sample. These may be used for genotyping
CC	This invention describes a novel immunogenic region (I) comprising an	CC	such as for disease mutation detection and for parentage determinations
CC	epitope of non-collagenous alpha-3 chain domain of type IV collagen which	CC	in humans and other animals), pathogen detection and identification and
CC	has intact cysteine residues. The epitope is located in the amino	CC	differential gene expression. The present sequence represents a
CC	terminal end of alpha3 chain and is recognized by circulating	CC	Mycobacterium tuberculosis capture oligonucleotide.
CC	autoantibodies (A) from a Goodpasture's patient. The product of the	XX	Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;
CC	cells producing (A) with an epitope-toxin complex, (I) is used for in	SQ	Query Match 66.0%; Score 13.2%; DB 12; Length 25;
CC	vitro determination (A) in a body fluid by contacting it with the	Best Local Similarity 83.3%; Pred. No. 1.5e-04;	
CC	immunogenic polypeptide molecule or a recombinant nucleic acid and	Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0	
CC	determination can also be done by contacting the body fluid with anti-		
CC	idiotypic antibodies and determining antigen-antibody reaction by		
CC	physical or chemical methods. (I) is also used in therapy for treating		
CC	Goodpasture's syndrome. AAZ8901-289440 represent primers used in the		
CC	isolation of the products of the invention		
XX		XX	RESULT 24
SQ	Sequence 23 BP; 4 A; 6 C; 7 G; 6 T; 0 U; 0 Other;	AAFA6591/C	
Query Match	66.0%; Score 13.2%; DB 3; Length 23;	ID AAFA6591	standard; DNA; 15 BP.
Best Local Similarity	83.3%; Pred. No. 1.5e+04;	XX	
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	AC AAFA6591;	
Qy	2 ACTCTTGAGGAAGGGCGC 19	XX	30-MAR-2001 (first entry)
Db	6 ACTTTGAGCACTGTC 23	DE	IGFBP3 oligonucleotide #11.
XX		XX	
XX		XX	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX		XX	cytostatic; dermatologic; cardiotonic; viricide; ophthalmologic; keloid;
XX		XX	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX		XX	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX		XX	Growth factor mediated cell proliferation; ichthyosis; serborrhoea; rubra;
AC	ADH72962;	XX	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX	ADH72962;	XX	hypernervouscular condition; hyperplasia; kidney disease;
DT	25-MAR-2004 (first entry)	XX	neovascular condition of the retina; ss.
XX		XX	
DE	M. tuberculosis capture oligonucleotide #70.	OS	Homo sapiens.
XX		XX	WO200078341-A1.
KW	ss; single nucleotide polymorphism; SNP detection; genotyping;	PN	
KW	pathogen detection; pathogen identification.	XX	
KW	Mycobacterium tuberculosis.	PD	28-DEC-2000.

DR WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.
 XX PS Example 7; Page 44; 201PP; English.
 XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAP45151 and AAP45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, rubra, pilasis, seborrhoea, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
 XX Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
 XX Query Match 65.0%; Score 13; DB 4; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 GCAGGAAGGGCT 20
 Db 15 GCAGGAAGGGCT 3

RESULT 27
 ADP14476 standard; DNA; 25 BP.

XX ID ADP14476;
 XX DT 26-AUG-2004 (first entry)
 XX DE Renal cell carcinoma differentially expressed gene probe #881.
 XX KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
 XX peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
 XX head/neck cancer; differential expression; probe.
 XX OS Homo sapiens.
 XX PN WO2004048933-A2.
 XX PD 10-JUN-2004.
 XX PP 21-NOV-2003; 2003WO-US037481.
 XX PR 21-NOV-2002; 2002US-0427982P.
 XX PR 03-APR-2003; 2003US-0459782P.

PA (AMHP) WYETH.
 PA (TWIN/) TWINE N C.
 PA (BURC/) BURCZNSKI M E.
 PA (TREP/) TREPICCHIO W L.
 PA (DORN/) DORNER A.
 PA (STOVR/) STOVER J A.
 PA (SLON/) SLONI D K.
 XX TWINE NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
 PI Sloni DK;
 XX DR WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing PT differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
 XX PS Disclosure; SEQ ID NO 1212; 350PP; English.
 XX The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample is a whole blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples isolated at different stages of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method of the invention.
 XX SQ Sequence 25 BP; 8 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
 XX Query Match 65.0%; Score 13; DB 12; Length 25;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 TCTTGAGGAAAGC 16
 Db 6 TCTTGAGGAAAGC 18
 RESULT 28
 ABSS9220
 ID ABSS9220 standard; DNA; 26 BP.
 XX AC ABSS9220;
 XX DT 05-NOV-2002 (first entry)
 XX DE Human G-protein coupled receptor, probe #123.
 XX KW Human; G-protein coupled receptor; GPCR; cardiomopathy; atherosclerosis; diabetes; cell signal processing; metabolic pathway modulation; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus Cancer; asthma; immune response; neurodegenerative disorder; inflammatory disorder; Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy; probe; ss.
 XX OS Homo sapiens.
 XX PN WO20025913-A2.
 XX PD 01-AUG-2002.
 XX PF 18-DEC-2001; 2001WO-US049394.
 XX PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-025743P.
 PR 10-JAN-2001; 2001US-0261718P.
 PR 12-JAN-2001; 2001US-0261498P.
 PR 24-JAN-2001; 2001US-0261689P.
 PR 08-FEB-2001; 2001US-0261746P.
 PR 22-FEB-2001; 2001US-0277021P.
 PR 14-MAR-2001; 2001US-0277946P.
 PR 23-MAR-2001; 2001US-027150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0288718P.
 PR 19-JUN-2001; 2001US-029327P.

PR 16-AUG-2001; 2001US-0312902P.
 XX (CURA-) CURAGEN CORP.
 XX Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA; Casman SJ, Vernet CAM, Shanyov SG, Gusev V, Malyankar UM, Edinger S; Gerlach V, Smithson G, Stone DJ, Sciore P, Macdougall JR, Gunther E; Peyman JA, Ellerman K, Gangoli EA, Millet I; DR WPI; 2002-599789/64.

XX New G protein coupled receptor polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer in humans.

XX Claim 1; Page 652; 685pp; English.

XX The invention relates to novel isolated G-protein coupled receptor (GPCR) polypeptides and polynucleotides. The GPCR polypeptides, GPCR nucleic acid and antibody are useful for treating, preventing or alleviating a GPCR-associated disorder or a pathological state in a subject, particularly a human. In particular, the disorder is cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell signal processing and metabolic pathway modulation. The GPCR polypeptide and nucleic acid are also useful for diagnosing the presence of or predisposition to a disease associated with altered levels of GPCR. Particularly cancer. The GPCR nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for disorders associated with aberrant GPCR expression or activity. The DNA encoding the protein is useful in gene therapy for treating the above conditions. Furthermore, the nucleic acids and polypeptides are useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, neurodegenerative disorders, asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or Albright hereditary osteodystrophy. These are also useful in developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. ABSS8747-ABSS5231 represent human GPCR coding sequences, primers and probes of the invention

XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

XX Query Match 65.0%; Score 13; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAAGAAC 16
 Db 3 TCTTGCAAGAAC 15

RESULT 29
 ABT04530 ID ABT04530 standard; DNA; 26 BP.
 XX AC ABT04530;
 XX DT 25-SEP-2002 (first entry)

XX Human G-protein coupled receptor probe SEQ ID NO: 473.

DE Human G-protein coupled receptor; GPCR; developmental disease; immune disease; retinal disease; metabolic disorder; feeding disorder; wasting disorder; infection; cancer; allergy; neurological disorder; antidiabetic; cardiant; antiatherosclerotic; probe; 88.

KW Homo sapiens.

PN WO20025558-A2.

XX PD 18-JUL-2002.

XX XX transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;

XX PR 18-DBC-2000; 2000US-0256635P.
 PR 21-DBC-2000; 2000US-0256876P.
 PR 04-FAN-2001; 2001US-025743P.
 PR 10-FAN-2001; 2001US-0260718P.
 PR 12-FAN-2001; 2001US-0261498P.
 PR 24-FAN-2001; 2001US-0261689P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0276150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-028718P.
 PR 19-JUN-2001; 2001US-0293327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX (CURA-) CURAGEN CORP.

XX PI Padigaru M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA; Malyankar UM, Edinger S; Gerlach V, Vernet CAM, Shanyov SG, Gusev V, Malyankar UM, Edinger S; Sciore P, Macdougall JR, Gunther E; Peyman JA, Ellerman K, Millet I, Tchernev VT, Anderson DW, Wolenc A; DR WPI; 2002-500840/53.

XX New G-protein coupled receptor polypeptides, encoding nucleic acids and immunospecific antibodies, useful for treating cardiomyopathy, atherosclerosis, diabetes or disorder related to cell signal processing and metabolic pathway modulation.

XX PT Example 3; Page 457; 473pp; English.

XX The present invention provides the protein and coding sequences of human G-protein coupled receptors designated GPCRx. These can be used in the development of developmental diseases, immune diseases, retinal diseases, metabolic disorders, feeding disorders, wasting disorders, infections, cancer, allergies, neurological disorders, behavioural disorders and reproductive disorders. The present sequence is a probe used to isolate a coding sequence of the invention. The sequence is modified at the 5' end by TET and at the 3' end by TAMRA

XX SQ Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

XX Query Match 65.0%; Score 13; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAAGAAC 16
 Db 3 TCTTGCAAGAAC 15

RESULT 30
 ABT05715 ID ABT05715 standard; DNA; 26 BP.
 XX AC ABT05715;
 XX DT 16-OCT-2002 (first entry)

XX DE GPCR related probe SEQ ID No 168.

XX KW Antidiabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCRX; anti-parkinsonian; cardiant; anti-arteriosclerotic; immunosuppressive; hypotensive; hemostatic; antifertility; antiasthmatic; antiinflammatory; anti-HIV; G-protein coupled receptor X; cardiomopathy; atherosclerosis; diabetes; metabolic disorder; diabetes; obesity; infectious disease; anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidemia; Parkinson's disorder; immune disorder; haemopoietic disorder; obesity; metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasia; congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma; transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;

KW	hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;	XX	AC	ADH31280;
KW	graft versus host disease; AIDS; bronchial asthma; Crohn's disease;	XX	AC	
KW	multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;	XX	DT	11-MAR-2004 (first entry)
XX		XX	DE	Human G-protein coupled receptor (GPCR) cDNA probe #107.
OS	Unidentified.	XX	XX	
PN	WO200246229-A2.	XX	XX	Human; G-protein coupled receptor; GPCR; ss; GPCRX; cardiomyopathy;
XX	PD 13-JUN-2002.	XX	XX	atherosclerosis; diabetes; obesity; infection; cancer;
PP	05-DEC-2001; 2001WO-US046530..	XX	XX	Alzheimer's disease; Parkinson's disease; asthma; allergy; hypertension;
XX	PR 05-DEC-2000; 2000US-0251459P.	XX	XX	retinal disease; urinary retention; angina pectoris; Crohn's disease;
PR	29-DEC-2000; 2000US-025907P.	XX	XX	schizophrenia; manic depression; probe.
PR	04-DEC-2001; 2001US-00005041.	XX	XX	Homo sapiens.
PA	(CURA-) CURAGEN CORP.	XX	XX	
XX	Casman SJ, Padigaru M, Burgess CB, Shimkets RA, Spytek KA,	XX	PN	US2003232332-A1.
PI	Gilbert JA, Mayotte JE, Baumgartner JC, Mishra V, Vernet CAM;	XX	PP	18-DEC-2001; 2001US-00024212.
PI	Dickinson KS, Ballinger RA, Wolenc AR;	XX	XX	
DR	WPI; 2002-537559/57.	XX	XX	
XX	Novel isolated G-protein coupled receptor polypeptide, designated NovX, useful for treating or preventing in human receptor-associated disorders e.g. cardiomypathy, atherosclerosis or diabetes.	XX	XX	
PT	PT	XX	XX	
PT	Example 2; Page 221; 264pp; English.	XX	XX	
PS	CC	XX	XX	The invention relates to a novel isolated G-protein coupled receptor X (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide and the antibody of the isolated protein is useful for treating or preventing a GPCRX-associated disorder in a subject, preferably human, where the disorder is cardiomypathy, atherosclerosis or diabetes. The isolated protein, its encoding polynucleotide and the antibody of the isolated protein is useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorder, Alzheimer's disease, various disorders and various disorders, immune disorders, haematopoietic disorders, and various disorders associated with obesity, the metabolic syndrome X, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with chronic diseases, and cancer. The disorders also include cardiomypathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, subaortic stenosis, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostrate cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer, fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease, and multiple sclerosis and cancer. The isolated protein, its encoding polynucleotide and the antibody of the isolated protein is useful in screening assays, detection assays (e.g., chromosomal mapping, tissue typing, forensic biology). The isolated polynucleotide is useful in gene therapy, to express the isolated protein, to detect GPCRX mRNA or a genetic lesion in a GPCRX gene, and to modulate GPCRX activity. The cell of the invention is useful for producing non-human transgenic animals. This polynucleotide sequence represents a probe of a GPCRX protein of the invention
CC	CC	XX	XX	
CC	CC	XX	XX	Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;
CC	CC	XX	XX	Query Match 65.0%; Score 13; DB 6; Length 26;
CC	Best Local Similarity 100.0%; Pred. No. 1.9e-04;	XX	XX	Best Local Similarity 100.0%; Pred. No. 1.9e-04;
CC	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	4 TCTTGAGGAGC 16	XX	XX	Padigaru M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA;
ID	3 TCTTGAGGAGC 15	XX	XX	Colman SD, Vernet CAM, Shenoy SG, Gusev VY, Malyankar UM;
Db		XX	XX	Edinger SR, Gerlach V, Smithson G, Stone DJ, Sciole P;
		XX	XX	Macdougall JR, Gunther E, Peyman JA, Ellerman K, Millet I;
		XX	XX	Tchernev VT, Anderson DW, Wolenc AR;
		XX	XX	WPI; 2004-061267/06.
		XX	XX	New G-protein coupled receptor (GPCR) polypeptides and nucleic acids, useful for diagnosing, preventing or treating GPCR-associated disorders, e.g. cardiomypathy, atherosclerosis or diabetes, and in pharmacogenomics.

XX Example 3; SEQ ID NO 472; 328pp; English.

PS The invention relates to human G-protein coupled receptor (GPCR) polypeptides and the polynucleotides encoding them, designated GPCRX. The invention also relates to a vector comprising a GPCRX nucleic acid, a cell comprising the vector, an antibody that binds immunospecifically to a GPCRX polypeptide, methods for determining the presence or amount of the polypeptide or the nucleic acid molecule in a sample, methods for identifying an agent that binds to or modulates the expression or activity of a polypeptide and a method for modulating the activity of the preventing or treating GPCRX associated disorders, such as cardiomopathy, atherosclerosis, diabetes, obesity, infections, cancer, Alzheimer's disease, Parkinson's disease, asthma, allergies, hypertension, retinal diseases, urinary retenion, angina pectoris, Crohn's disease, schizoprenia and manic depression. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The polypeptides are also useful as vaccines or as immunogens to produce antibodies. This sequence represents a probe which hybridises to human GPCRX cDNA of the invention.

XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

SQ Query Match 65.0%; Score 13; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 TCTTGAGGAGC 16
Db 3 TCTTGAGGAGC 15

RESULT 32
ADK98351.C
ID ADK98351 standard; DNA; 24 BP.
AC ADK98351;
XX 06-MAY-2004 (first entry)
DE Primer of the invention #4071.
KW human; single nucleotide polymorphism; SNP; ss; primer.
XX Synthetic.
PS JPP003259875-A.
PN 16-SEP-2003.
PD 08-MAR-2002; 2002JP-00064373.
XX 08-MAR-2002; 2002JP-00064373.
PR (RAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA WPI; 2004-093977/10.
XX Novel polynucleotide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.

PS SEQ ID NO 7380; 2627pp; Japanese.

XX The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.

Sequence 24 BP; 5 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;

XX Query Match 64.0%; Score 12.8; DB 12; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTTTGGGAAAC 16
Db 19 GACTCTAGGGCAC 4

RESULT 33
AC AC12520 standard; DNA; 25 BP.
ID AC12520
AC AC12520;
XX 13-OCT-2003 (first entry)
DT 13-OCT-2003
DB Human microarray DNA oligonucleotide SEQ ID NO 12511.
KW EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
XX Homo sapiens.
OS XX
PN US2003104410-A1.
XX PD 05-JUN-2003.
XX PP 15-MAR-2002; 2002US-00098263.
XX PR 16-MAR-2001; 2001US-0276759P.
PA (AFFY-) AFFYMATRIX INC.
PI Mittmann MP;
XX DR WPI; 2003-567953/53.
XX New array of nucleic acid probes, useful for in situ hybridization, in PT Southern, Northern or dot-blot hybridization to identify or detect the PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 12511; 9PP; English.
XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
XX SQ Sequence 25 BP; 11 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;	Indels 0; Gaps 0;	Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;	Indels 0; Gaps 0;
Qy 4 TCTTGAGGAAAGGGC 19		Qy 2 ACTCTGCAGGAAGCG 17	
Db 2 TCTTGAGGAAAGTGGC 17		Db 3 ACTTGAGGAACCG 18	
RESULT 36			
ACH53400			
ID ACH53400 standard; DNA; 25 BP.			
XX			
AC ACH53400;			
XX			
DT 16-OCT-2003 (first entry)			
XX			
DE DNA target sequence #2536 useful in array for genetic analyses.			
XX			
KW Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR primer; ss.			
XX			
KW Unidentified.			
XX			
OS US2003082596-A1.			
PN			
XX			
PD 01-MAY-2003.			
XX			
PF 08-AUG-2002; 2002US-00215112.			
XX			
PR 08-AUG-2001; 2001US-0311040P.			
XX			
(MITT/) MITTMANN M.			
PA			
XX			
DR WPI; 2003-576608/54.			
XX			
New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.			
PT PS ID NO 2536; 9pp; English.			
XX			
Claim 1: SEQ ID NO 2536; 9pp; English.			
CC The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probe may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH50865-ACH5260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipspdbntry.html			
CC XX			
CC Sequence 25 BP; 6 A; 5 C; 5 G; 9 T; 0 U; 0 Other;			
CC SQ 64.0%; Score 12.8; DB 2; Length 25;			
CC Query Match 64.0%; Score 12.8; DB 2; Length 27;			
CC Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;			
CC Db 8 CTTGAGGAAAGCGCT 23			
CC RESULT 37			
AAK22793			
ID AAK22793 standard; DNA; 27 BP.			
XX			
AC AAK22793;			
XX			
DT 27-MAY-1999 (first entry)			
XX			
DE PCR primer 84672.			
XX			
KW Protein-enveloped polyribonucleic acid; viral RNA; bacteriophage RNA; diagnostic; detection; assay; PCR primer; ss.			
XX			
KW Synthetic.			
OS			
PN DE19737442-A1.			
XX			
PD 04-MAR-1999.			
XX			
PP 97DE-01037442.			
XX			
PR 97DE-01037442.			
XX			
(OLfE-) OLfERT LANDT TIB MOLBIOL SYNTHESELABOR.			
PA			
XX			
PI Landt O;			
XX			
DR WPI; 1999-168279/15.			
XX			
PT Genetically modified RNA viruses or bacteriophages - useful as RNA standards, positive controls, etc.			
XX			
PS Example 5; col 15; 12pp; German.			
XX			
CC This invention describes protein-enveloped polyribonucleic acids containing viral RNA or bacteriophage RNA, characterised in that the natural nucleic acid sequence is varied. Also described is a method for producing a protein-enveloped polyribonucleic acid. Protein-enveloped polyribonucleic acids are useful as standards for diagnostic methods in which the presence of a specific ribonucleic acid is detected, and are useful as standard or competitor sequences for methods in which the amount of a defined ribonucleic acid is determined. They are also useful as positive controls for the detection of viral RNA, where the protein-enveloped polyribonucleic acid is added directly to the assay sample and is isolated in parallel with the viral RNA. They can monitor the efficiency of processes for purifying nucleic acids or the efficiency of the reverse transcription of ribonucleic acids, and are useful as comparison substances in assays in which nucleic acids are detected by hybridisation or in assays in which nucleic acids are detected after or during nucleic acid amplification. They are useful as carriers for RNA sequences having a functional property, and for mixtures of RNA sequences from which individual RNA sequences can be selected			
CC XX			
CC Sequence 27 BP; 9 A; 6 C; 6 G; 6 T; 0 U; 0 Other;			
CC SQ 64.0%; Score 12.8; DB 2; Length 27;			
CC Query Match 64.0%; Score 12.8; DB 2; Length 27;			
CC Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;			
CC Db 8 CTTGAGGAAAGCGCT 23			
CC RESULT 38			
CC SQ 64.0%; Score 12.8; DB 2; Length 25;			
CC Query Match 64.0%; Score 12.8; DB 2; Length 27;			
CC Best Local Similarity 87.5%; Pred. No. 2.4e+04; Matches 14; Conservative 0; Mismatches 2;			
CC Db 8 CTTGAGGAAAGCGCT 23			

PA (UYTY) UNIV TOKYO.
 XX
 PI Nakamura Y, Katagiri T;
 XX
 DR WPI; 2004-3305/30.

PT Diagnosing pancreatic cancer (PNC) comprises determining a level of expression of a PNC-associated gene in a patient derived biological sample.

XX

PS Example 1; SEQ ID NO 13; 152pp; English.

XX The present invention describes a method for diagnosing pancreatic cancer (PNC) or a predisposition to developing PNC in a subject. The method comprises determining a level of expression of a PNC-associated gene in a patient derived biological sample, where an increase or decrease of the level compared to a normal control level of the gene indicates that the subject suffers from or is at risk of developing PNC. Also described: (1) a PNC reference expression profile, comprising a pattern of gene expression of two or more genes, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (2) a method of screening for a compound for treating or preventing PNC or malignant PNC; (3) a kit comprising a detection reagent which binds to two or more nucleic acid sequences, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906 or the encoded polypeptides; (4) an array comprising two or more nucleic acids which bind to one or more nucleic acid sequences, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (5) a method of treating or preventing PNC in a subject; (6) a composition, for treating or preventing PNC, comprising a pharmaceutical amount of: (a) an antisense polynucleotide or small interfering RNA against a polyuridylate, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-893; (b) an antibody or antibody fragment that binds to a protein encoded by any one gene, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-893; or (c) the compound obtained by the method of (2) as an active ingredient and a pharmaceutical carrier; and (7) a method of predicting recurrence of PNC. The compounds have cytostatic activity, and can be used in vaccines and in gene therapy. The method is useful in diagnosing PNC or a predisposition to developing PNC in a subject. The methods, compounds and compositions are useful in treating or preventing PNC. The polypeptides are useful as vaccines against PNC. The present sequence represents a reverse transcription (RT) PCR primer used in semi-quantitative RT-PCR experiments related to the diagnosis of PNC, which is used in an example from the present invention.

XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match Score 12.6; DB 12; Length 20;
 Best Local Similarity 63.0%; Pred. No. 3e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGGAAGGGCT 20

Db 20 AATCTCCGAAAGCTGCT 2

Search completed: December 3, 2005, 13:29:58
 Job time : 419 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:03:26 ; Search time 3651 Seconds

Title: US-10-773-678A-342
 Perfect score: 20
 Sequence: 1 gacttgcaggaaaggcggt 20

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database :	EST:*			
*	1: 9b_est1:*			
*	2: 9b_est2:*			
*	3: 9b_est3:*			
*	4: 9b_htc:*			
*	5: 9b_est4:*			
*	6: 9b_est5:*			
*	7: 9b_est6:*			
*	8: 9b_est7:*			
*	9: 9b_gss1:*			
*	10: 9b_gss2:*			
*	11: 9b_gss3:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
- 1	11.4	57.0	25	6 CB412589	
2	11.4	57.0	28	CB412564	ScaE_0880
3	11.1	55.0	30	10 C2477398	AZ633273
C 4	10.8	54.0	30	2 BF209105	AZ633273
C 5	10.8	54.0	30	8 DN955287	AZ633273
C 6	10.6	53.0	20	9 A2314365	AZ633273
C 7	10.6	53.0	24	11 TA273GQ7Q	AZ633273
C 8	10.6	53.0	26	12 A6222081	AZ633273
C 9	10.6	53.0	28	1 A895705	AZ633273
10	10.6	53.0	28	10 CL6633977	AZ633273
11	10.6	53.0	30	1 AL045592	AZ633273
12	10.6	53.0	30	1 AL045336	AZ633273
13	10.6	53.0	30	1 AL045352	AZ633273
14	10.6	53.0	30	1 AL045477	AZ633273
15	10.6	53.0	30	1 AL045487	AZ633273
C 16	10.6	53.0	30	1 AL0450912	AZ633273
17	10.4	52.0	23	11 TA278H12P	AZ633273
18	10.4	52.0	24	9 A2468735	AZ633273
C 19	10.4	52.0	28	1 A1429345	AZ633273
C 20	10.4	52.0	29	9 A2472735	AZ633273
21	10.4	52.0	29	9 A2771858	AZ633273
22	10.4	52.0	29	9 BH849150	SALK_0693

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
- 1	11.4	57.0	25	6 CB412589	ScaE_0880
2	11.4	57.0	28	CB412564	AZ633273
3	11.1	55.0	30	10 C2477398	AZ633273
C 4	10.8	54.0	30	2 BF209105	AZ633273
C 5	10.8	54.0	30	8 DN955287	AZ633273
C 6	10.6	53.0	20	9 A2314365	AZ633273
C 7	10.6	53.0	24	11 TA273GQ7Q	AZ633273
C 8	10.6	53.0	26	12 A6222081	AZ633273
C 9	10.6	53.0	28	1 A895705	AZ633273
10	10.6	53.0	28	10 CL6633977	AZ633273
11	10.6	53.0	30	1 AL045592	AZ633273
12	10.6	53.0	30	1 AL045336	AZ633273
13	10.6	53.0	30	1 AL045352	AZ633273
14	10.6	53.0	30	1 AL045477	AZ633273
15	10.6	53.0	30	1 AL045487	AZ633273
C 16	10.6	53.0	30	1 AL0450912	AZ633273
17	10.4	52.0	23	11 TA278H12P	AZ633273
18	10.4	52.0	24	9 A2468735	AZ633273
C 19	10.4	52.0	28	1 A1429345	AZ633273
C 20	10.4	52.0	29	9 A2472735	AZ633273
21	10.4	52.0	29	9 BH849150	SALK_0693

RESULT 1

CB412589

LOCUS

ScaE_0880

DEFINITION

Bay scallop Uni-ZAP XR Expression Library Argopecten irradians cDNA 5' similar to Argopecten irradians cDNA library, unknown mRNA sequence.

ACCESSION

CB412589

VERSION

EST.

KEYWORDS

Argopecten irradians

Argopecten irradians

Bivalvia

Pectinidae

Metazoa

Mollusca

Bivalvia

Pectinomorpha

Pectinidae

Unpublished (2003)

JOURNAL

COMMENT

Experimental Marine Biology Laboratory (EMBL)

Institute of Oceanology, Chinese Academy of Science (IOCAS)

7 Nanhai Road, Qingdao, Shandong 266071, P. R. China

Tel: +86-0532-288552

Email: lishong@qdio.ac.cn

Seq Primer: M13 Forward

Location/Qualifiers

1..25

/organism="Argopecten irradians"

/mol_type="mRNA"

/db_xref="taxon:31199"

/sex="hermaphrodite"

/tissue_type="whole body"

/dev_stage="maturation phage"

/clone_id="Bay scallop Uni-ZAP XR Expression Library"

/note="Organ: whole body; Vector: pBluescript (+/-); Site: Xhol; Site 2: EcoRI; Using Stratagene's Uni-ZAP XR cDNA synthesis Kit; we constructed a cDNA library of Bay scallop." 4975 ESTs were gained."

ORIGIN

Query Match

57.0%

Score 11.4;

DB 6;

Length 25;

Best Local Similarity 92.3%;

Matches 12;

Conservative 0;

Mismatches 1;

Indels 0;

Gaps 0;

Origin

7 TGCAAGAACGGCGC 19

ALIGNMENTS

Tan, L.R., Ventura, R., Woo, A., Zakralsk, I., Zhao, L., Chen, F.J., Swimmer, C., Kopozynski, C., Duyk, G., Winberg, M.L., and Margolis, J.	A complementary transposon tool kit for <i>Drosophila melanogaster</i>
RESULT 2 CBA12564	LOCUS DEFINITION CB412564 28 bp mRNA linear EST 01-JAN-2005 ScAE 0852 Bay scallop Uni-ZAP XR Expression Library Argopecten irradians CDNA 5', similar to Argopecten irradians cDNA library, unknown, mRNA sequence.
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	GI:56934125 EST. Argopecten irradians Argopecten irradians Eukarya; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinoidea; Pectinidae; Argopecten. 1 (bases 1 to 28) Song, L., Xu, W., Li, H., Wu, L., Xiang, J. and Guo, X. The construction and EST analysis of cDNA library from bay scallop Argopecten irradians Unpublished (2003)
JOURNAL COMMENT	Contact: Longtao Wu Experimental Marine Biology Laboratory (EMBL) Institute of Oceanology, Chinese Academy of Science (IOCAS) 7 Nanhai Road, Qingdao, Shandong 266071, P. R. China Tel: +86-0532-2888552 Email: lshsong@qdio.ac.cn Seq primer: M13 Forward Location/Qualifiers 1..28 /organism="Argopecten irradians" /mol_type="mRNA" /db_xref="txon:31199" /sex="hermaphrodite" /tissue_type="whole body" /dev_stage="maturation phage" /clone_lib="Bay scallop Uni-ZAP XR Expression Library" /note="Organ: whole body; Vector: pBluescript's Uni-ZAP XR cDNA synthesis Kit"; we constructed a cDNA library of Bay scallop. 4975 ESTs were gained."
FEATURES SOURCE ORIGIN	Query Match Score 57.0%; Best Local Similarity 92.3%; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 3 CZ477398	LOCUS DEFINITION CZ477398 30 bp DNA linear GSS 29-APR-2005 Drosophila melanogaster P element XP insertions <i>Drosophila</i> <i>melanogaster</i> genomic Sequence recovered from 3' end of P element, Genomic survey sequence.
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	GI:62972730 Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukarya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Phydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 30)
REFERENCE AUTHORS	Singh, C.M., Buchholz, R.R., Demsky, M., Pawson, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Green, R., Hartouni, S.R., Howie, E., Jakubala, L., Stevens, T.M., Stuber, C., Laufer, A., Mazzoni, J., Smith, R.D., Unpublished (1999)
COMMENT	1 (bases 1 to 30) Tissue Procurement: ATCC CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILY) DNA Sequencing by: Incyte Genomics, Inc. Clone Submission: MGC clone distribution information can be

ound through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

ORIGIN	adapted vector DNA, and transformed into chemically-competent <i>E. coli</i> XL1-Gold (Stratagene) cells and selected for ampicillin resistance."	SOURCE	Mus musculus (house mouse)
Query Match	53.0% Score 10.6; DB 9; Length 20;	ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Best Local Similarity	76.5%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;	REFERENCE	Sciurognathi: Murioidea; Muridae; Murinae; Mus.
Matches	13; Conservative	AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingay, A., von Niederhäusern, A., and Wright, D., Weiss, R.
Qy	4 TCTTGAGGAGGGCT 20	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Db	20 TCCTCCAGGAAGCAGT 4	JOURNAL	unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@gene.tics.utah.edu		
RESULT 7	TA273G07Q/c	FEATURES	High quality sequence stop: 26. Location/Qualifiers
LOCUS	TA273G07Q 24 bp DNA linear GSS 13-DEC-2000	source	1..26
DEFINITION	T. brucei sheared genomic DNA clone 273g07, reverse sequence, genomic survey sequence.	organism	"Mus musculus"
ACCESSION	AL487649	mol_type	"genomic DNA"
VERSION	AL487649.1	strain	"C57BL/6J"
KEYWORDS	GI:11852459	db_xref	"taxon:10090"
SOURCE	GSS.	clone	"UUGC1M0455E10"
ORGANISM	Trypanosoma brucei	sex	"Male"
REFERENCE	1. (bases 1 to 24) Hall, N., Bowman, S., Lennard, N.J., Doggett, J.J., Atkin, R., Chillingworth, C., Ormond, D., El-Sayed, N., Hou, L., Meilwies, S.E., Rajandream, M.A. and Barrell, B.G.	lab_host	" <i>E. coli</i> strain XL1-Gold, Tr-resistant, F-"
AUTHORS	Direct Submission	/clone	lib="Mouse 10kb plasmid UUGC1M library"
VERSION	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhs@sanger.ac.uk	note	"Vector: PWD42hv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/shares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi 4732114 gb AF129072), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent <i>E. coli</i> XL1-Gold (Stratagene) cells and selected for ampicillin resistance."
KEYWORDS	2. (bases 1 to 24) Constructed at the Institute for Genomic Research (TIGR). Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nebsayed@igr.org	ORIGIN	Query Match 53.0%; Score 10.6; DB 11; Length 24; Best Local Similarity 76.5%; Pred. No. 2.e+06; Mismatches 0; Indels 0; Gaps 0;
SOURCE	3. (bases 1 to 24) Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ . Location/Qualifiers	Query Match 53.0%; Score 10.6; DB 9; Length 26; Best Local Similarity 76.5%; Pred. No. 2.1e+06; Mismatches 0; Indels 0; Gaps 0;	
FEATURES	4. (bases 1 to 24) /organism="Trypanosoma brucei" /mol_type="genomic DNA" /strain="TREU927" /db_xref="taxon:5691" /clone="#273g07"	Query Match 53.0%; Score 10.6; DB 9; Length 26; Best Local Similarity 76.5%; Pred. No. 2.1e+06; Mismatches 0; Indels 0; Gaps 0;	
ORIGIN	Query Match 53.0%; Score 10.6; DB 11; Length 24; Best Local Similarity 76.5%; Pred. No. 2.e+06; Mismatches 0; Indels 0; Gaps 0;		
Query	1 GACTCTGCGAGAACCG 17	RESULT 9	AA895705
Db	18 GATCATTCGGAAGCG 2	LOCUS	AA895705
KEYWORDS	24 TCTTGCACTGAGCAGTT 8	DEFINITION	AA895705_v14402.rl Stratagene mouse macrophage (#937306) Mus musculus cDNA clone IMAGE:1295427 5' similar to SW:DIAG_HUMAN P49189 ALDEHYDE DEHYDROGENASE, B3 ISOZYME ; mRNA sequence.
RESULT 8	AZ622081/c	ACCESSION	AA895705_v14402.rl
LOCUS	AZ622081	VERSION	AA895705_v14402.rl Stratagene mouse macrophage (#937306) Mus musculus cDNA clone IMAGE:1295427 5' similar to SW:DIAG_HUMAN P49189 ALDEHYDE DEHYDROGENASE, B3 ISOZYME ; mRNA sequence.
DEFINITION	IM0455E10R	KEYWORDS	AA895705
ACCESSION	IM0455E10R	VERSION	AA895705
VERSION	AZ622081.1	KEYWORDS	AA895705
KEYWORDS	SSS.		

RESULT 12
 AL045336 LOCUS DKFZP43A095_r1_434 (synonym: htes3) Homo sapiens mRNA linear EST 06-JUL-2004
 DEFINITION DKFZP43A095, mRNA sequence.
 ACCESSION AL045336
 VERSION 1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES source Location/Qualifiers
 1 .30
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZP43A095"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /Clone_Lib="H434" (synonym: htes3)"
 /note="vector: pSport1; Site_1: NotI; Site_2: SalI"

** ORIGIN
 Query Match 53.0%; Score 10.6%; DB 1; Length 30;
 Best Local Similarity 76.5%; Pred. No. 2.1e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 • * QY 2 ACTCTGCAAGGAAGCGG 18
 Db 5 ACGCTGCAAGTACCGG 21

RESULT 13
 AL045352 LOCUS DKFZP43A075_r1_434 (synonym: htes3) Homo sapiens mRNA linear EST 06-JUL-2004
 DEFINITION DKFZP43A075, mRNA sequence.
 ACCESSION AL045352
 VERSION AL045352.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES source Location/Qualifiers
 1 .30
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZP43A075"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /Clone_Lib="H434" (synonym: htes3)"
 /note="vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
 Query Match 53.0%; Score 10.6%; DB 1; Length 30;
 Best Local Similarity 76.5%; Pred. No. 2.1e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

• * QY 2 ACTCTGCAAGGAAGCGG 18
 Db 5 ACGCTGCAAGTACCGG 21

RESULT 14
 AL045477 LOCUS DKFZP434H225_r1_434 (synonym: htes3) Homo sapiens mRNA linear EST 06-JUL-2004
 DEFINITION DKFZP434H225, mRNA sequence.
 ACCESSION AL045477
 VERSION AL045477.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES source Location/Qualifiers
 1 .30
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZP434H225"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /Clone_Lib="H434" (synonym: htes3)"
 /note="vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
 Query Match 53.0%; Score 10.6%; DB 1; Length 30;
 Best Local Similarity 76.5%; Pred. No. 2.1e+06;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

• * QY 2 ACTCTGCAAGGAAGCGG 18
 Db 5 ACGCTGCAAGTACCGG 21

RESULT 15
 AL045487 LOCUS DKFZP434I105_r1_434 (synonym: htes3) Homo sapiens mRNA linear EST 06-JUL-2004
 DEFINITION DKFZP434I105, mRNA sequence.
 ACCESSION AL045487
 VERSION AL045487.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE EST (Duesterhoeft, et al.)

JOURNAL	Unpublished (1999)		
COMMENT	Contact: MIPS		
FEATURES			
Source			
1..30	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DFK2p341105" /tissue_type="testis" /dev_stage="adult" /lab_host="DIL0B" /clone_id="134" (synonym: htes3)" /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"		
ORIGIN			
Query Match	53.0%; Score 10.6; DB 1; Length 30; Best Local Similarity 76.5%; Pred. No. 2.1e+06; Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
Db			
2 ACTCTTGACGAAGCCG 18 5 ACGCTTGAGGTACCG 21			
RESULT 16			
AJ650912/c	AJ650912 CSQRAN19 <i>Sus scrofa</i> cDNA clone C0003276_101, mRNA DEFINITION sequence.		
LOCUS	18 bp linear EST 07-JUL-2004		
DEFINITION	AJ650912 CSQRAN19 <i>Sus scrofa</i> cDNA clone C0003276_101, mRNA sequence.		
ACCESSION	AJ650912		
VERSION	EST.		
KEYWORDS	GI:49327757		
SOURCE			
ORGANISM	<i>Sus scrofa</i> (pig)		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.			
REFERENCE			
AUTHORS	Anderson,S.I., Finlayson,H.A. and Archibald,A.L.		
TITLE	Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Anderson SI Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UNITED KINGDOM Single pass sequencing. Bases called and trimmed with phred v0.020425.C Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector: pBlueScriptII KS+ R. SiteI: EcoRI R. Site2: NotI 5'. Seq Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.		
FEATURES			
Source			
1..18	/organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:9623" /clone="C0003276_101" /tissue_type="ovary" /clone_id="CSQRAN19" /note="Vector: pBlueScriptII (KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"		
ORIGIN			
Query Match	52.0%; Score 10.4; DB 1; Length 18; Best Local Similarity 91.7%; Pred. No. 2.5e+06; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Db			
1 GCAGCTAGGGC 1			
RESULT 17			
TA278H12P	TA278H12P <i>T. brucei</i> sheared genomic DNA clone 278h12, forward sequence,		
LOCUS	23 bp linear GSS 13-DEC-2000		
DEFINITION	<i>T. brucei</i> sheared genomic DNA clone 278h12, forward sequence,		
ACCESSION	AU485533		
VERSION	1 GI:11851598		
KEYWORDS	GSS.		
SOURCE			
ORGANISM	<i>Trypanosoma brucei</i> <i>Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;</i> <i>Trypanosoma.</i>		
1..(bases 1 to 23)			
REFERENCE			
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J.J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.		
COMMENT			
JOURNAL	Submitted (10-DEC-2000) <i>Trypanosoma brucei</i> genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk		
FEATURES			
Source			
1..23	/organism="Trypanosoma brucei" /mol_type="genomic DNA" /strain="TRE0927" /db_xref="taxon:5691" /clone="278h12"		
ORIGIN			
Query Match	52.0%; Score 10.4; DB 11; Length 23;		
LOCUS	Best Local Similarity 91.7%; Pred. No. 2.6e+06;		
DEFINITION	Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
VERSION	AZ468735		
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus (house mouse)		
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.			
RESULT 18			
AZ468735	AZ468735 Mouse 10kb plasmid UGC1M 1 library Mus musculus genomic clone UGC1M0281114R, genomic survey sequence.		
LOCUS	24 bp linear GSS 04-OCT-2000		
DEFINITION	1MO281114R		
VERSION	AZ468735		
KEYWORDS			
SOURCE			
ORGANISM			
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Sciurognathi; Muroidea; Muridae; Murinae; Mus.			
REFERENCE			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.		
COMMENT			
JOURNAL	8 GCAGAAAGGGCC 19		

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1732
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of A₂₉₄₀₇₆₀.

Class: TDNA tagged.

FEATURES

Location/Qualifiers

1 .29
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html"

ORIGIN

Query Match 52.0%; Score 10.4%; DB 9; Length 29;
 Best Local Similarity 70.0%; Pred. No. 2.6e-06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ORIGIN

	Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1 GACTCTGGAGGAACGGGT 20	52.0%	10.4;	DB 10;	70.0%	2.6e+06;	0;	0;	0;
Db	8 GACTCTGGAAACACCT 27	30	mRNA						

ORIGIN

	Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1 GACTCTGGAGGAACGGGT 20	52.0%	10.4;	DB 10;	70.0%	2.6e+06;	0;	0;	0;
Db	23 GTCTTTCTGGAGCTGCTGCT 4	30	linear						

ORIGIN

	Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1 GACTCTGGAGGAACGGGT 20	52.0%	10.4;	DB 10;	70.0%	2.6e+06;	0;	0;	0;
Db	23 GTCTTTCTGGAGCTGCTGCT 4	30	mRNA						

ORIGIN

	Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1 GACTCTGGAGGAACGGGT 20	52.0%	10.4;	DB 10;	70.0%	2.6e+06;	0;	0;	0;
Db	23 GTCTTTCTGGAGCTGCTGCT 4	30	linear						

ORIGIN

	Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1 GACTCTGGAGGAACGGGT 20	52.0%	10.4;	DB 10;	70.0%	2.6e+06;	0;	0;	0;
Db	23 GTCTTTCTGGAGCTGCTGCT 4	30	mRNA						

/organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="C0428.1"
 /db_xref="Taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci. USA, 98: 8709-8713."

investigated regulatory sequences in noncoding human DNA that are associated with repression of an integrated human immunodeficiency virus type 1 (HIV-1) promoter. HIV-1 integration results in the formation of precise and homogeneous junctions between viral and host DNA, but integration takes place at many locations. Thus, the variation in HIV-1 gene expression at different integration sites reports the activity of regulatory sequences at nearby chromosomal positions. Negative regulation of HIV transcription is of particular interest because of its association with maintaining HIV in a latent state in cells from infected patients. To identify chromosomal regulators of HIV transcription, we infected Jurkat T cells with an HIV-based vector transducing green fluorescent protein (GFP) and separated cells into populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profiling. Low-level GFP expression correlated with integration in (i) gene deserts, (ii) centromeric heterochromatin, and (iii) very highly expressed cellular genes. These data provide a genome-wide picture of chromosomal features that repress transcription and suggest models for transcriptional latency in cells from HIV-infected patients."

ORIGIN	Query Match	Score 52.0%; Best Local Similarity 70.0%; Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	DB 3; Pred. No. 2.7e+06; (bases 1 to 20)	Length 30; Score 10.4; DB 3; Length 30; (bases 1 to 20)	SOURCE Mus musculus (house mouse)	ORGANISM Mus musculus
					Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Mus.	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
					REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamm, C., Islam, H., Longacre, S., Mahmoud, M., Meenin, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A. and Wright, D. Weiss, R.	Scutrognathi; Muroidae; Murinae; Mus.
					AUTHORS	(bases 1 to 20)
					TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
RESULT 25					JOURNAL	Unpublished (2000)
LOCUS CD532073/c	CD532073	19 bp mRNA	linear EST 31-DEC-2003	COMMENT Contact: Robert B. Weiss	COMMENT	University of Utah Genome Center
DEFINITION 13104 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA 3', mRNA sequence.	CD532073	EST	CDNA	University of Utah	University	Rm. 303B, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
ACCESSION CD532073	CD532073.1	GI:40452085	EST.	84112, USA	TeL:	801 585 5606
VERSION					Fax:	801 585 7177
SOURCE					Email:	ddunn@genetics.utah.edu
ORGANISM Arabidopsis thaliana (thale cress)					Insert Length:	10000 Std Error: 0.00
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					Plate:	0497 row: D column: 20
REFERENCE Guo, Y., Cai, Z. and Gan, S.					Seq primer:	CGTGTAAGAACGCCAGT
AUTHORS					Class:	Plasmid ends
TITLE Transcriptome of Arabidopsis leaf senescence					High quality sequence stop:	20.
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)					Location/Qualifiers	
COMMENT Contact: Susheng Gan, Tel: 607 254 5418 Fax: 607 255 0599 Email: sg28@cornell.edu Insert Length: 19 Std Error: 0.00 Seq primer: T7 POLYA=No.					1..20	
					/organism="Mus musculus"	/organism="Mus musculus"
					/mol_type="genomic DNA"	/mol_type="genomic DNA"
					/strain="C57BL/6J"	/strain="C57BL/6J"
					/note="vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male)"	/note="vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male)"
					/clone="UFGCIM049/D20"	/clone="UFGCIM049/D20"
					/sex="Male"	/sex="Male"
					/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-
					/clone_lib="Mouse 10kb plasmid UFGCIM library"	/clone_lib="Mouse 10kb plasmid UFGCIM library"
					/note="vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male)"	/note="vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male)"
					Laboratory Mouse DNA Resource	Laboratory Mouse DNA Resource
					(http://www.jax.org/resources/documents/dnares/)	(http://www.jax.org/resources/documents/dnares/)
					The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1 4732 14 gb AF139072.1), a copy-number inducible derivative of Plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1 4732 14 gb AF139072.1), a copy-number inducible derivative of Plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN	Query Match	Score 51.0%; Best Local Similarity 80.0%; Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	DB 6; Pred. No. 3.1e+06; (bases 1 to 20)	Length 19; Score 10.2; DB 6; Length 19; (bases 1 to 20)	ORIGIN	Query Match
					Best Local Similarity 80.0%; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 80.0%; Mismatches 0; Indels 0; Gaps 0;
					Score 10.2; DB 9; Length 20; Pred. No. 3.2e+06; (bases 1 to 20)	Score 10.2; DB 9; Length 20; Pred. No. 3.2e+06; (bases 1 to 20)
RESULT 26	Query Match	Score 51.0%; Best Local Similarity 80.0%; Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	DB 6; Pred. No. 3.1e+06; (bases 1 to 20)	Length 19; Score 10.2; DB 9; Length 20; Pred. No. 3.2e+06; (bases 1 to 20)	DEFINITION	Query Match
LOCUS A2637794/c	A2637794	20 bp DNA linear GSS 13-DEC-2000	DNA	22 bp mRNA	RESULT 27	Query Match
DEFINITION 1M0497D0F	Mouse 10kb plasmid UFGCIM library	Mus musculus genomic	linear	mRNA	AA915121	Query Match
ACCESSION A2637794	Mouse 10kb plasmid UFGCIM library	Genomic survey sequence.			LOCUS AA915121	Best Local Similarity 80.0%; Mismatches 0; Indels 0; Gaps 0;
VERSION GSS.					DEFINITION V203905.r1 Soares' mammary gland NbMMG Mus musculus cDNA clone IMAGE:1314676 5' similar to TR:Q15765 Q15765 VHL BINDING PROTEIN-1	DEFINITION V203905.r1 Soares' mammary gland NbMMG Mus musculus cDNA clone IMAGE:1314676 5' similar to TR:Q15765 Q15765 VHL BINDING PROTEIN-1
KEYWORDS					ACCESSION AA915121	ACCESSION AA915121

VERSION	AA915121.1	GI:	3054513					
SOURCE	Mus musculus (house mouse)							
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath; Muroidea; Murinae; Mus.							
REFERENCE	1 (bases 1 to 27)							
AUTHORS	Kawamoto, S., Okubo, K., Yoshiii, J., Katsuki, M. and Matsubara, K.							
TITLE	Analysis of gene expression in mouse embryogenesis by 3'-directed cDNA sequencing							
JOURNAL	Unpublished (1995)							
COMMENT	Contact: Shoko Kawamoto Institute for Cellular and Molecular Biology Osaka University 1-3, Yamadoka, Suita, Osaka, 565, Japan Email: shoko@next.iicmb.osaka-u.ac.jp.							
FEATURES	source							
	1	27						
	/organism="Mus musculus"							
	/mol_type="mRNA"							
	/strain="C57BL/6J"							
	/db_xref="Caxon:1.0090"							
	/clone="md0789"							
	/tissue:type="decidua tissue (day 6.5-8.5 of gestation)"							
	/clone_idb="Mouse 3'-directed"							
ORIGIN								
	Query Match	51.0%						
	Best Local Similarity	80.0%						
	Matches	12;	Conservative	0;	Mismatches	3;	Indels	0;
	Gaps	0;						
RESULT	29							
LOCUS	CZ475704							
DEFINITION	d07387-5prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.							
ACCESSION	CZ475704							
KEYWORDS	GI:62969731							
SOURCE	GSS.							
ORGANISM	Drosophila melanogaster (fruit fly)							
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephemeroidea; Drosophilidae; Drosophila.								
REFERENCE	1 (bases 1 to 27)							
AUTHORS	Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Dembsky,M., Fawcett,R.D., Stevens,L.M., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Laufer,A., Hartooni,S.R., Howie,E., Jakkula,L., Joo,D., Kilpatrick,K., Tan,L.R., Mazzotta,J., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.I., and Margolis,J.J.							
TITLE	A complementary transposon tool kit for Drosophila melanogaster using P and PiggyBac							
JOURNAL	Nat. Genet.	36 (3)	, 283-287 (2004)					
PUBMED	14981521							
COMMENT	Contact: Roger A. Hoskins Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA Tel: 510 486 4015 Fax: 510 486 6798 Email: Rhoskins@lbl.gov							
SEQUENCE	Sequence recovery method was inverse PCR.							
ORIENTATION	Orientation is forward strand relative to 5' end of P element.							
EST POSITION	The P element insertion position is 20 in the 27 bases. This insertion position refers to the first base of the 8 base target recognition sequence.							
CLASS	transposon insertion site.							

FEATURES	Location/Qualifiers	ORIGIN	be found at http://signal.salk.edu/tDNA_protocols.html "
	1. .27 /organism="Drosophila melanogaster" /mol type="genomic DNA" /strain="isogenic w- strain" /db_xref="taxon:7227" /clone lib="Exelixis P element XP insertions" /note="Vector: P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinsky balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."		
ORIGIN			
	Query Match 51.0%; Score 10.2; DB 10; Length 27; Best Local Similarity 80.0%; Pred. No. 3.3e+06; Matches 0; Mismatches 3; Indels 0; Gaps 0;		
	Qy 5 CTTGCAGGAAGGGC 19 Db 13 CTCGAAAGGAAAGGCC 27		
BZ595262/c	BZ595262 29 bp DNA linear GSS 07-JAN-2003		
DEFINITION	Arabidopsis thaliana genomic clone SALK_086337.15..90..n, genomic survey sequence.		
ACCESSION LOCUS	BZ595262		
VERSION	BZ595262.1 GI:27535781		
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyt; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1 (bases 1 to 29)		
AUTHORS	Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Becker, J.R.		
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Becker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 1010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu		
FEATURES	This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g25580. Class: TDNA tagged.		
source	1..29	/organism="Arabidopsis thaliana" /mol type="genomic DNA" /ecotype="Col-0" /db_xref="taxon:3702" /clone="SALK_086337.15..90..n" /clone lib="Arabidopsis thaliana TDNA insertion lines" /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can	
ORIGIN	Query Match 51.0%; Score 10.2; DB 9; Length 29; Best Local Similarity 80.0%; Pred. No. 3.3e+06; Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
DEFINITION	4 TCTTGAGGAAGCGG 18 Db 18 TCTTGAGGAGCCGG 4		
ACCESSION LOCUS	AZ506426		
VERSION	AZ506426		
KEYWORDS	GSS,		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eutheriontiglires; Glires; Rodentia; Sciurognathia; Muroidea; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 27)		
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacons, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahoud, N., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA tel: 801 585 5606 fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0347 row: M column: 04 Seq primer: CACAGGGAAACAGCTATGACC Class: plasmid ends		
FEATURES	High quality sequence stop: 27. Location/Qualifiers 1..27		
source	/organism="Mus musculus" /mol type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="C57BL/6J" /lab host="E. Coli strain XN10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UGCLM library" /note="Vector: pW42nv. Purified genomic DNA from M, musculus C57BL/6J (male), was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnare/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 473214 gb AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into		

ORIGIN	Query	Match	Score 10;	DB 9;	Length 27;
	Best Matches	Local Similarity	50.0%; 72.2%;	Pred. No. 4.1+06;	
	13;	Conservative	0; Mismatches	5;	Indels 0; Gaps 0
Qy	1	GACITCTTGAGGAAGGG	1.8		
Db	5	GGCTGTTGAGGAAGGG	22		

to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

KEYWORDS	GSS Drosophila melanogaster (fruit fly)	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
SOURCE	Drosophila melanogaster	1 (bases 1 to 22)
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
REFERENCE	1 (bases 1 to 30)	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
AUTHORS	Rhinehart,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Denkby,M., Fawcett,R., Francis-Jang,H.L., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Greer,K., Hartouni,S.R., Horie,E., Jakkula,L., Joo,D., Killpack,K., Laurer,A., Mazzotta,J.J., Smith,R.D., Stevens,L.M., Stubber,C., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.I., and Margolis,J.	Unpublished (1997)
TITLE	A complementary transposon tool kit for <i>Drosophila melanogaster</i> using P and PIGGYBAC	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov
JOURNAL	Nat. Genet. 36 (3), 283-287 (2004)	This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
PUBMED	14981521	Trace considered overall poor quality
COMMENT	Contact: Roger A Hoskins Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94120, USA Tel: 510 486 4015 Fax: 510 486 6798 Email: RHoskins@lbl.gov	Insert Length: 566 Std Error: 0.00 Seq primer: -40mm13 fwd. Et from Amersham High quality sequence stop: 1.
FEATURES	source	Location/Qualifiers 1..22 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone=IMAGE:1521650" /lab_host="DH10B" /clone_lib="Soares_NFL_T_GBC_S1" /note="Organ: pooled; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL9W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.B. clones 297480-302087, 682652-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN		
		Query Match 49 0% Score 9.8; DB 1; Length 22; Best Local Similarity 84.6%; Pred. No. 5e+06; Matches 11; Conserv 0; Mismatches 2; Indels 0; Gaps 0;
		/note="Vector: P element XP (Exelixis) P element XP insertion" /clone_lib="Exelixis P element XP (Genbank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinsky balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
FEATURES	source	Location/Qualifiers 1..30 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /strain="isogenic w- strain" /db_xref="taxon:7227" /clone_lib="P element XP (Exelixis) P element XP insertion" /note="Vector: P element XP (Genbank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinsky balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
ORIGIN		
		Query Match 49 0% Score 9.8; DB 1; Length 22; Best Local Similarity 84.6%; Pred. No. 5e+06; Matches 11; Conserv 0; Mismatches 2; Indels 0; Gaps 0;
		RESULT 36 AZ660103/c LOCUS A2660103 27 bp DNA linear GSS 14-DEC-2000 DEFINITION 1M0538B01F Mouse 10kb plasmid TUGC1M0538B01 F, genomic survey sequence clone TUGC1M0538B01 F, genomic survey sequence
		ACCESSION A2660103 VERSION A2660103.1 GI:11797249 KEYWORDS GSS SOURCE Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
		REFERENCE 1 (bases 1 to 27) AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenah,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederauer,A. and Wright,D., Weiss,R. COMMENT Unpublished (2000)
RESULT	35 AA912871 LOCUS AA912871_1 GI:3052263	Title: Robert B. Weiss Journal: University of Utah Genome Center
DEFINITION	AA912871_1 Soares NFL T GBC_S1 Homo sapiens cDNA clone IMAGE:1524650_3, similar to TR:Q92506 Q92506 A MEMBER OF THE SHORT-CHAIN ALCOHOL DEHYDROGENASE FAMILY ; mRNA sequence.	Unpublished (2000)
ACCESSION	AA912871	AA912871_1 GI:3052263
VERSION	EST.	University of Utah
SOURCE	Homo sapiens (human)	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
ORGANISM	Homo sapiens	84112, USA tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0538 row: B column: 01
 Seq primer: CGTTCTAAACGACGCCAGT
 Class: Plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1. 27.

FEATURES source
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGCIM0538B01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid TUGCIM library"
 /note="Vector: PWD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match Score 9.8; DB 9; Length 27;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query 7 TGCGAGAACGGC 19
 Db 19 TGCGAGAACGGC 7

RESULT 37
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 DEFINITION ac27e01.s1 Stratagene ovary (#37217) Homo sapiens CDNA clone mRNA
 Sequence.
 AA633771.1 GI:2556985
 EST.
 Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Bacteria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo
 1 (bases 1 to 28)
 Hillier,L., Allan,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Frizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
 Martin,J., Moore,B., Schellenbach,K., Sceptoce,M., Tan,F.,
 Theising,B., White,Y., Wylie,T., Waterston,R., and Wilson,R.
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1632169"

Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert Length: 709 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:857688"
 /sex="Female"
 /dev_stage="49 year old"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene ovary (#37217)"
 /note="Organ: ovary; Vector: Bluescript SK; Site: 1: EcoRI; Site 2: XbaI; Cloned unidirectionally. Primer: Öligo dT. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR vector; ~5' adaptor sequence: 5' GAATTCGCAACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."
 ORIGIN
 Query Match Score 9.8; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Query 7 TGCGAGAACGGC 19
 15 TGCGAGAACGGC 3

RESULT 38
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 DEFINITION ou60b01.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632169_3,
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 sequence.
 ACCESSION AI005184
 VERSION AI005184.1 GI:3214694
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo
 1 (bases 1 to 28)
 REFERENCE NCBI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbcp/image/Image.html
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 Seq primer: primer name ambiguous
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1632169"

/sex="female, pooled"
/tissue_type="Breast"
/lab host="DH10B"
/clone lib="NCI CGAP Br2"
/noe="Vector: PT735-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI CGAP Br1. Library was constructed by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 TTGCAGGAGCCG 18
Db 1 TTGAAAGAGCCG 13

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 TTGCAGGAGCCG 18
Db 1 TTGAAAGAGCCG 13

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAACTGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'

/clone lib="NCI CGAP Br2"
/noe="Vector: PT735-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI CGAP Br1. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 TTGCAGGAGCCG 18
Db 1 TTGAAAGAGCCG 13

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 TTGCAGGAGCCG 18
Db 1 TTGAAAGAGCCG 13

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TGCAGGAGCCG 19
Db 15 TGTAGAAGAGGC 3

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAACTGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'

Search completed: December 3, 2005, 15:07:09

Mon Dec 5 07:58:23 2005

us-10-773-678a-342.max30.rst

Page 18

Job time : 3655 secs

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	Issued Patents NA:*
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	5: /cgn2_6/pcodata/1/ina/H COMB seq:*
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	8: /cgn2_6/pcodata/1/ina/RE COMB seq:*
	9: /cgn2_6/pcodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	14.8	74.0	25	3 US-09-396-196G-124305	Sequence 124305, Sequence 65325, A
c 2	14.2	71.0	25	3 US-09-396-196G-65325	Sequence 19, Appl
c 3	14	70.0	20	3 US-09-388-451-19	Sequence 13, Appl
c 4	13.8	69.0	28	3 US-09-358-881-19	Sequence 42438, AP
c 5	13.6	68.0	25	3 US-09-349-3439	Sequence 6, Appl
c 6	13.6	68.0	25	3 US-09-396-196G-42438	Sequence 40794, A
c 7	13.6	68.0	23	3 US-09-396-444-6	Sequence 65314, A
c 8	13.2	66.0	25	3 US-09-396-40794	Sequence 88577, A
c 9	13.2	66.0	25	3 US-09-396-196G-63314	Sequence 134, APP
c 10	13.2	66.0	25	3 US-09-396-196G-63314	Sequence 134, APP
c 11	13.2	66.0	25	3 US-09-396-196G-88577	Sequence 26683, A
c 12	12.8	66.0	25	3 US-09-396-196G-26683	Sequence 26685, A
c 13	12.8	64.0	20	3 US-09-396-196G-26685	Sequence 107676,
c 14	12.8	64.0	20	3 US-09-396-196G-107676	Sequence 107677,
c 15	12.8	64.0	20	3 US-09-396-196G-107677	Sequence 107678,
c 16	12.8	64.0	20	3 US-09-396-196G-107678	Sequence 107679,
c 17	12.8	64.0	25	3 US-09-396-196G-107679	Sequence 108203,
c 18	12.8	64.0	25	3 US-09-396-196G-107679	
c 19	12.8	64.0	25	3 US-09-396-196G-107679	
c 20	12.8	64.0	25	3 US-09-396-196G-107679	
c 21	12.8	64.0	25	3 US-09-396-196G-107679	
c 22	12.8	64.0	25	3 US-09-396-196G-107679	
c 23	12.8	64.0	25	3 US-09-396-196G-107679	
c 24	12.8	64.0	25	3 US-09-396-196G-107679	

ALIGNMENTS

RESULT 1
US-09-396-196G-124305/C
US-09-396-196G-124305

; Sequence 124305, Application US/09396196G
; Patent No. 6821724;
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101..1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 124305
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-124305

RESULT 2
US-09-396-196G-65325
US-09-396-196G-65325
; Sequence 65325, Application US/09396196G
; Patent No. 6821724;
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101..1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 124305
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-65325

NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-65325

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Best Local Similarity 84.2%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 3
US-09-288-461-19
; Sequence 19, Application US/09288461
; Patent No. 6159694
; GENERAL INFORMATION:
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; NUMBER OF SEQ ID NOS: 107
; CURRENT APPLICATION NUMBER: US/09/288,461
; FILE REFERENCE: ISPH-0338
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-288-461-19

Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-758-881-19
; Sequence 19, Application US/09758881
; Patent No. 6720764
; GENERAL INFORMATION:
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; NUMBER OF SEQ ID NOS: 152
; CURRENT APPLICATION NUMBER: US/09/758,881
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 152
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-758-881-19

Query Match 70.0%; Score 14; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAA 14
Db 7 GACTCTTGAGGAA 20

RESULT 5
US-08-137-134B-13
; Sequence 13, Application US/08137134B
; Patent No. 6369038
; GENERAL INFORMATION:
; APPLICANT: BLUMENFELD, Marcia
; APPLICANT: BRANDYS, Paschal
; APPLICANT: D'AURIO, Luc
; APPLICANT: VASSEUR, Marc
; TITLE OF INVENTION: CLOSED SENSE AND ANTISENSE OLIGONUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,134B
; FILING DATE: 23-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/05114
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PLAYER, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58359
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 393-5350
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-137-134B-13

Query Match 69.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGGGC 19
Db 12 CTCTTGCAGGAAGGGC 28

RESULT 6
US-09-396-196G-3439/c
; Sequence 3439, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart

```

; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3439
; LENGTH: 25
; TYPE: DNA
; ORGANISM: MUS musculus
; US-09-396-196G-3439

Query Match      68 0%;  Score 13.6;  DB 3;  Length 25;
Best Local Similarity 80.0%;  Pred. No. 1.4e+03;
Matches 16;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;
Qy          1 GACTCTTGAGGAACGGCT 20
                  ||||| ||||| ||||| ||||| ||||| 2
Db          21 GAACCTTGTGGCAGCTGCT 2
                  ||||| ||||| ||||| ||||| ||||| 2

RESULT 7
US-09-396-196G-42438
Sequence 42438, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 42438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: MUS musculus
; US-09-396-196G-42438

Query Match      68 0%;  Score 13.6;  DB 3;  Length 25;
Best Local Similarity 80.0%;  Pred. No. 1.4e+03;
Matches 16;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;
Qy          1 GACTCTTGAGGAACGGCT 20
                  ||||| ||||| ||||| ||||| ||||| 2
Db          4 GACTCTTGAGGAACGGCT 23
                  ||||| ||||| ||||| ||||| ||||| 2

RESULT 8
US-09-496-444-6-/C
Sequence 6, Application US/09496444
; Patent No. 6933276
; GENERAL INFORMATION:
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon Kamm, William J.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Bailey, Matthew A.
; TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide,
; TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide,
; FILE REFERENCE: 1109
; CURRENT APPLICATION NUMBER: US/09/496,444
; CURRENT FILING DATE: 2000-02-02
; EARLIER APPLICATION NUMBER: US 60/119,857
; EARLIER FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/101,551
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(723)
; US-09-496-444-6

Query Match      66 0%;  Score 13.2;  DB 3;  Length 23;
Best Local Similarity 83.3%;  Pred. No. 2.2e+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;
Qy          3 CTCCTGCAGGAACGGCT 20
                  ||||| ||||| ||||| ||||| ||||| 2
Db          19 CTGTCGAGCAAGCGGT 2
                  ||||| ||||| ||||| ||||| ||||| 2

RESULT 9
US-09-396-196G-40794/C
Sequence 40794, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 40794
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-40794

Query Match      66 0%;  Score 13.2;  DB 3;  Length 25;
Best Local Similarity 83.3%;  Pred. No. 2.3e+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;
Qy          3 CTCCTGCAGGAACGGCT 20
                  ||||| ||||| ||||| ||||| ||||| 2
Db          20 CTATGGCTGGAAACGGGT 3

RESULT 10
US-09-396-196G-65314
Sequence 65314, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

```

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 65314
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-65314

Query Match 66.0%; Score 13.2; DB 3; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 13
 US-09-081-385-134
 Sequence 88577, Application US/09396196G
 Patent No. 6593436
 GENERAL INFORMATION:
 APPLICANT: Getanaga, T.
 ATTORNEY/AGENT: Granger, G.A.
 TITLE OF INVENTION: Factors Altering Tumor Necrosis Factor Receptor Releasing Enzyme Activity, and Methods
 NUMBER OF SEQUENCES: 154
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSEQ For Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/081.385
 FILING DATE: 06-NOV-1996
 PRIORITY NUMBER: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 88577
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-88577

Query Match 66.0%; Score 13.2; DB 3; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
 US-09-396-196G-88577
 Sequence 88577, Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 ATTORNEY/AGENT: David Mack
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/110,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 88577
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-88577

Query Match 66.0%; Score 13.2; DB 3; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 12
 US-09-396-196G-88578
 Sequence 88578, Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 ATTORNEY/AGENT: David Mack
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/110,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 88578
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-88578

Query Match 66.0%; Score 13.2; DB 3; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.3e+03; Indels 0; Gaps 0;

RESULT 14
 US-09-52-639-134
 Sequence 134, Application US/09752639
 Patent No. 6911314
 GENERAL INFORMATION:
 APPLICANT: Getanaga, T.
 ATTORNEY/AGENT: Granger, G.A.
 TITLE OF INVENTION: Factors Altering Tumor Necrosis Factor Receptor Releasing Enzyme Activity, and Methods
 TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods

TITLE OF INVENTION: of use thereof
 NUMBER OF SEQUENCES: 154
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94104-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FASTSEQ for Windows Ver
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/752,639
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US99/1079
 FILING DATE:
 APPLICATION NUMBER: 09/081,385
 FILING DATE:
 APPLICATION NUMBER: 08/964,747
 FILING DATE: 05-NOV-1997
 APPLICATION NUMBER: 60/030,761
 FILING DATE: 06-NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: W.L. Frank
 REGISTRATION NUMBER: 41,386
 REFERENCE/DOCKET NUMBER: 22000-200
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEX: 650-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IS-09-752-639-134
 Query Match 64.0% Score 1
 Best Local Similarity 87.5% Pred. N
 Matches 14; Conservative 0; Misma
 GENERAL INFORMATION:
 4 TCTTGGCGAACGGC 19
 1 ||||| |||||
 1 TCTTCGGGAGCTGC 16
 Ry
 Db
 RESULT 15
 IS-09-712-813-124
 Sequence 134, Application US/09/712813
 Patent No. 6910084
 GENERAL INFORMATION:
 APPLICANT: Gatanaga, T.
 CRANGER, G.A.
 TITLE OF INVENTION: Factors Alte
 Factor Recip
 NUMBER OF SEQUENCES: 154
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94104-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows Version 2.0b
 SOFTWARE: FastSEQ for Windows

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/712,813
 FILING DATE: 13 -No. 6910084-2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/081,385
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/964,747
 FILING DATE: 05 -NOV-1997
 APPLICATION NUMBER: 60/030,761
 FILING DATE: 06 -NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Wu, Frank
 REGISTRATION NUMBER: 41,386
 REFERENCE/DOCKET NUMBER: 22000-20577-21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792

INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 134:

US-09-712-813-134

Query	TCCTGCACGGAAGGGC 19	Score 64.0% ;	DB 3 ;	Len 6
Best Local Similarity	87.5% ;	Pred. No. 3 .5e+03 ;		
Matches	14 ;	Mismatches 0 ;		
	Conservative	2 ;		
Db	TCTCCAGGAAGTGC 16			

RESULT 16
 US-09-700-354A-134

/ Sequence 134, Application US/09700354A
 / Patent No. 6955894

GENERAL INFORMATION:
 APPLICANT: Gatanaga, Tetsuya
 Grange, Gale A.

TITLE OF INVENTION: Factors Altering Tumor Necrosis Factor Receptor Releasing Enzyme

NUMBER OF SEQUENCES: 154

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP
 STREET: 200 MIDDLEFIELD ROAD, #200
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/700,354A
 FILING DATE: 17 -Apr-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/081,385
 FILING DATE: 14 -MAY-1998
 APPLICATION NUMBER: PCT/US99/10793
 FILING DATE: 14 -MAY-1999

ATTORNEY/AGENT INFORMATION:
 NAME: Francis, Ceilo L.
 REGISTRATION NUMBER: 36,513

REFERENCE/DOCKET NUMBER: IRVN-007CIP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-327-3400
 TELEFAX: 650-327-3231
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 134:
 US-09-700-354A-134

Query Match 64.0%; Score 12.8; DB 3; Length 20;
 Best Local Similarity 87.5%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGAGGAGGGC 19
 ||||| ||||| |||||
 Db 1 TCTTCAGGAGCTGC 16

RESULT 17
 US-09-396-196G-26683/c
 Sequence 26683, Application US/09396196G
 ; GENERAL INFORMATION:
 ; Patent No. 6821724
 ; Prior Application Number: 107676
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; PRIORITY FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 26683
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-396-196G-26683

Query Match 64.0%; Score 12.8; DB 3; Length 25;
 Best Local Similarity 87.5%; Pred. No. 3.6e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGAGGAGGGC 19
 ||||| ||||| |||||
 Db 25 TCGTCAGGAGGGC 10

RESULT 18
 US-09-396-196G-26684/c
 Sequence 26684, Application US/09396196G
 ; GENERAL INFORMATION:
 ; Patent No. 6821724
 ; Prior Application Number: 107676
 ; APPLICANT: Michael Mittmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/09/396,196G
 ; PRIORITY FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 26684
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 US-09-396-196G-26684

Query Match 64.0%; Score 12.8; DB 3; Length 25;
 Best Local Similarity 87.5%; Pred. No. 3.6e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy   1 GACTCTTGAGGAAGC 16
Db    ||||| | | | | | | | |
      25 GACTCTTGATGATGC 10

RESULT 21
US-09-396-196G-107677/C
; Sequence 107677, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Mittmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 107679
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-107677

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1 GACTCTTGAGGAAGC 16
Db    ||||| | | | | | | | |
      16 GACTCTTGATGATGC 1

RESULT 24
US-09-396-196G-108203/C
; Sequence 108203, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;   APPLICANT: Michael Mittmann
;   APPLICANT: David Mack
;   APPLICANT: David Lockhart
;   APPLICANT: Affymetrix, Inc.
;   TITLE OF INVENTION: Methods of Genetic Analysis
;   FILE REFERENCE: 3101.1
;   CURRENT APPLICATION NUMBER: US/09/396,196G
;   CURRENT FILING DATE: 1999-09-15
;   PRIOR APPLICATION NUMBER: 60/100,678
;   PRIOR FILING DATE: 1998-09-17
;   NUMBER OF SEQ ID NOS: 127806
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 108203
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-108203

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   5 CTTGGAGGAGGGCT 20
Db    ||||| | | | | | | | | | | | | | | | | | | | |
      17 CTTGGATGAGGGCTT 2

RESULT 25
US-09-972-115A-30
; Sequence 30, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
;   APPLICANT: Geron Corporation
;   APPLICANT: Gregg, Morin B.
;   APPLICANT: Waiber, Funk D.
;   APPLICANT: Miedzyzlaw, Piatuszek A.
;   TITLE OF INVENTION: A Second Mammalian Telomerase
;   FILE REFERENCE: 080/003C
;   CURRENT APPLICATION NUMBER: US/09/972,115A
;   CURRENT FILING DATE: 2001-10-05

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1 GACTCTTGAGGAAGC 16
Db    ||||| | | | | | | | |
      22 GACTCTTGATGATGC 7

RESULT 23
US-09-396-196G-107679/C
; Sequence 107679, Application US/09396196G
; Patent No. 6821724

```

PRIOR APPLICATION NUMBER: US 60/128,577
 PRIOR FILING DATE: 2000-04-10
 PRIOR APPLICATION NUMBER: US 60/129,123
 SEQ ID NO: 30
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Primer
 US-09-972-115A-30

Query Match Score 63.0%; Best Local Similarity 78.9%; Pred. No. 4.5e+03; Length 21;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGC 19
 Db 3 GACAAATTGCTGGAACTGTC 21

RESULT 26
 US-08-749-852-7
 ; Sequence 7, Application US/08749852
 ; Patent No. 5874222
 GENERAL INFORMATION:
 ; APPLICANT: JIRTLIE, RANDY L.
 ; APPLICANT: DE SOUZA, ANGUS T.
 ; APPLICANT: HANKINS, GERALD R.
 ; TITLE OF INVENTION: TUMOR SUPPRESSOR
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHVE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/749, 852
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: WILSON, MARY J.
 REGISTRATION NUMBER: 32,915
 REFERENCE/DOCKET NUMBER: 1579-104
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-749-852-7

Query Match Score 63.0%; Best Local Similarity 78.9%; Pred. No. 4.5e+03; Length 22;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGC 19
 Db 4 GACTGTTCCTGGAAAGCAGC 22

RESULT 27
 US-08-297-299B-86
 ; Sequence 86, Application US/08297299B
 ; Patent No. 5656427
 GENERAL INFORMATION:
 ; APPLICANT: Phillip Hammond and Anthony Endozo
 ; TITLE OF INVENTION: NUCLEIC ACID HYBRIDI-
 ZATION ASSAY PROBES,
 ; TITLE OF INVENTION: HELPER PROBES AND AMPLIFICATION OLIGO-
 ; TITLE OF INVENTION: NUCLEOTIDES TARGETED TO MYCOPLASMA PNEUMONIAE
 ; TITLE OF INVENTION: NUCLEIC ACID
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/297,299B
 FILING DATE: August 29, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: n/a
 FILING DATE: n/a
 ATTORNEY/AGENT INFORMATION:
 NAME: Heber, Sheldon O.
 REGISTRATION NUMBER: 38-179
 REFERENCE/DOCKET NUMBER: 208/130
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-297-299B-86

Query Match Score 63.0%; Best Local Similarity 78.9%; Pred. No. 4.5e+03; Length 23;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGC 19
 Db 5 GACTCTAGCAGGCAATGGC 23

RESULT 28
 US-08-858-083-86
 ; Sequence 86, Application US/08858083
 ; Patent No. 5969122
 GENERAL INFORMATION:
 ; APPLICANT: Phillip Hammond and Anthony Endozo
 ; TITLE OF INVENTION: NUCLEIC ACID HYBRIDI-
 ZATION ASSAY PROBES,

TITLE OF INVENTION: HELPER PROBES AND
 TITLE OF INVENTION: AMPLIFICATION OLIGO-
 NUCLEOTIDES TARGETED TO
 TITLE OF INVENTION: MYCOPLASMA PNEUMONIAE
 NUMBER OF SEQUENCES: 92
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Suite 4700
 STATE: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage

COMPUTER: IBM Comptible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/858,083

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/297,299

FILING DATE: August 29, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: 67-3510

INFORMATION FOR SEQ ID NO: 86:

LENGTH: 23

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-858-083-86

Query Match

Best Local Similarity

Score 12.6 ; DB 2 ;

Length 23 ;

Pred. No. 4.5e+03 ;

Indels 0 ;

Gaps 0 ;

Matches 15 ;

Conservative 0 ;

Mismatches 4 ;

Indels 0 ;

Gaps 0 ;

Qy 1 GACTCTGAGGAAGGGC 19

Db 5 GACTCTGAGGCATGGC 23

RESULT 30

US-08-866-108A-13006

Sequence 13006, Application US/09866108A

Patent No. 6686108

GENERAL INFORMATION:

PRIOR APPLICATION: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: HANZBL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wanhsing

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSTIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ABOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 66/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

COMPUTER READABLE FORM:

PRIOR FILING DATE: 2001-01-30
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 15755
 SOFTWARE: Aeomica Sequence Listing Engine

Patent No. 6686188
 SEQ ID NO 13006
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-866-108A-13006

Query Match 63.0%; Score 12.6; DB 3; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCT 20
 Db 7 AGTCCCTGCGAAAGGGCT 25

RESULT 31
 US-09-866-108A-13007
 Sequence 13007, Application US/09866108A
 Patent No. 6686188
 GENERAL INFORMATION:
 APPLICANT: JI, Yonggang
 APPLICANT: PENN, Sharron G.
 APPLICANT: HANZEL, David K.
 APPLICANT: RANK, David R.
 APPLICANT: CHEN, Wenshang
 APPLICANT: SHANNON, Mark
 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: GB 24263 . 6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2000-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
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 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
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 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 15755
 SOFTWARE: Aeomica Sequence Listing Engine

Patent No. 6686188
 SEQ ID NO 13007
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-866-108A-13007

Query Match 63.0%; Score 12.6; DB 3; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCT 20
 Db 6 AGTCCCTGCGAAAGGGCT 24

RESULT 32
 US-09-866-108A-13008
 Sequence 13008, Application US/09866108A
 Patent No. 6686188
 GENERAL INFORMATION:
 APPLICANT: JI, Yonggang
 APPLICANT: PENN, Sharron G.
 APPLICANT: HANZEL, David K.
 APPLICANT: RANK, David R.
 APPLICANT: CHEN, Wenshang
 APPLICANT: SHANNON, Mark
 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: GB 24263 . 6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2000-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
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 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 15755
 SOFTWARE: Aeomica Sequence Listing Engine

Patent No. 6686188
 SEQ ID NO 13007
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-866-108A-13009

Query Match 63.0%; Score 12.6; DB 3; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCT 20
 Db 5 AGTCCCTGCGAAAGGGCT 23

RESULT 33
 US-09-866-108A-13009
 Sequence 13009, Application US/09866108A
 Patent No. 6686188
 GENERAL INFORMATION:
 APPLICANT: JI, Yonggang
 APPLICANT: PENN, Sharron G.
 APPLICANT: HANZEL, David K.
 APPLICANT: RANK, David R.
 APPLICANT: CHEN, Wenshang
 APPLICANT: SHANNON, Mark
 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A
 CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: GB 24263 .6
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 15755
 SOFTWARE: Aeomica Sequence Listing Engine
 Patent No. 6686188
 SEQ ID NO 13009
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-866-108A-13009

Query Match 63.0%; Score 12.6; DB 3; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGGCT 20
 Db 3 AGTCCCTGCCAGAACGGCGCT 21

RESULT 34
 US-09-866-108A-13010
 / Sequence 13010, Application US/09866108A
 / Patent No. 6686188
 / GENERAL INFORMATION:
 / APPLICANT: GU, Yizhong
 / APPLICANT: JI, Yonggang
 / APPLICANT: PENN, Sharron G.
 / APPLICANT: HANZEL, David K.
 / APPLICANT: RANK, David R.
 / APPLICANT: CHEN, Wensheng
 / APPLICANT: SHANNON, Mark
 / TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 / FILE REFERENCE: AEOMICA-7
 / CURRENT APPLICATION NUMBER: US/09/866,108A
 / CURRENT FILING DATE: 2001-05-25
 / PRIOR APPLICATION NUMBER: US 60/207,456
 / PRIOR FILING DATE: 2000-05-26
 / PRIOR APPLICATION NUMBER: GB 24263 .6
 / PRIOR FILING DATE: 2000-10-04
 / PRIOR APPLICATION NUMBER: US 60/236,359
 / PRIOR FILING DATE: 2000-09-27
 / PRIOR APPLICATION NUMBER: PCT/US01/00666
 / PRIOR FILING DATE: 2001-01-30
 / PRIOR APPLICATION NUMBER: PCT/US01/00667
 / PRIOR FILING DATE: 2001-01-30
 / PRIOR APPLICATION NUMBER: PCT/US01/00664
 / PRIOR FILING DATE: 2001-01-30
 / PRIOR APPLICATION NUMBER: PCT/US01/00669
 / PRIOR FILING DATE: 2001-01-30
 / PRIOR APPLICATION NUMBER: PCT/US01/00665
 / PRIOR FILING DATE: 2001-01-30
 / PRIOR APPLICATION NUMBER: PCT/US01/00668
 / PRIOR FILING DATE: 2001-01-30
 / PRIOR APPLICATION NUMBER: PCT/US01/00663
 / PRIOR FILING DATE: 2001-01-30
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 15755
 / SOFTWARE: Aeomica Sequence Listing Engine
 / Patent No. 6686188
 / SEQ ID NO 13011
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-09-866-108A-13011

Query Match 63.0%; Score 12.6; DB 3; Length 25;
 Best Local Similarity 78.9%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 4;
 Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGGCT 20

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Db 2 AGTCCTGCAGAAGGGCT 20
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56156
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-56156

RESULT 36
; Sequence 13012, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/8666,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: SEO ID NOS: 15755
Patent No. 6686188
SEQ ID NO 13012
LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13012

Query Match 63.0%; Score 12.6%; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03; Mismatches 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Gaps 0;

Qy 2 ACTCTTGCGAGGAAGGGCT 20
Db 1 AGTCCTGCAGAAGGGCT 19
; Query Match 63.0%; Score 12.6%; DB 3; Length 25;
; Best Local Similarity 78.9%; Pred. No. 4.6e+03; Mismatches 4; Indels 0; Gaps 0;
; Matches 15; Conservative 0; Gaps 0;

Qy 2 ACTCTTGCGAGGAAGGGCT 20
Db 7 ACTCTTACGAAAGGGCT 25
; Query Match 63.0%; Score 12.6%; DB 3; Length 25;
; Best Local Similarity 78.9%; Pred. No. 4.6e+03; Mismatches 4; Indels 0; Gaps 0;
; Matches 15; Conservative 0; Gaps 0;

RESULT 38
US-09-449-335-8
; Sequence 8, Application US/09449335
; Patent No. 6303365
; GENERAL INFORMATION:
; APPLICANT: Busch, Marco
; APPLICANT: Hain, Rudiger
; APPLICANT: Marin, William
; APPLICANT: Tietjen, Klaus
; APPLICANT: Klori, Andreas
; TITLE OF INVENTION: Method of determining the activity of 1-deoxy-D-xylulose-5-phosphate reductoisomerase and 1-deoxy-D-xylulose-5-phosphate synthase
; TITLE OF INVENTION: Method of determining the activity of 1-deoxy-D-xylulose-5-phosphate reductoisomerase and 1-deoxy-D-xylulose-5-phosphate synthase
; FILE REFERENCE: 020US
; CURRENT APPLICATION NUMBER: US/09/449 ,335
; CURRENT FILING DATE: 1999-11-24
; EARLIER APPLICATION NUMBER: DE 199 35 967.9
; EARLIER FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-449-335-8

Query Match 63.0%; Score 12.6%; DB 3; Length 30;
Best Local Similarity 78.9%; Pred. No. 4.7e+03; Mismatches 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Gaps 0;

Qy 1 GACTCTTGCGAGGAAGGGCT 19
Db 8 GACTCATGATGACTGGC 26
; Query Match 63.0%; Score 12.6%; DB 3; Length 30;
; Best Local Similarity 78.9%; Pred. No. 4.7e+03; Mismatches 4; Indels 0; Gaps 0;
; Matches 15; Conservative 0; Gaps 0;

Qy 1 GACTCTTGCGAGGAAGGGCT 19
Db 8 GACTCATGATGACTGGC 26
; Query Match 63.0%; Score 12.6%; DB 3; Length 30;
; Best Local Similarity 78.9%; Pred. No. 4.7e+03; Mismatches 4; Indels 0; Gaps 0;
; Matches 15; Conservative 0; Gaps 0;

RESULT 39
US-08-171-718-77/C
; Sequence 77, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thoreef
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

RESULT 37
US-09-396-196G-56156
; Sequence 56156, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 310.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100, 678
; PRIOR FILING DATE: 1998-09-17

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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/171,718
 FILING DATE: 22-DEC-1993
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/108,808
 FILING DATE: 19-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/022,034
 FILING DATE: 25-FEB-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/026,063
 FILING DATE: 04-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Anne
 REGISTRATION NUMBER: 36,463
 REFERENCE/DOCKET NUMBER: 0609.3850003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-171-718-77

Query Match 62.0%; Score 12.4; DB 3;
 Best Local Similarity 92.9%; Pred. No. 5.6e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

Qy 3 CTCTTGAGGAGC 16
 Db 15 CTCTTGAGGTAGC 2

RESULT 40
 US-08-478-087-77/C
 Sequence 77, Application US/08478087
 Patent No. 6077685
 GENERAL INFORMATION:
 APPLICANT: Trofatter, James A.
 APPLICANT: MacCollin, Ma M.
 APPLICANT: Gusella, James F.
 TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-2934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/478,087
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/171,718
 FILING DATE: 22-DEC-1993
 APPLICATION NUMBER: US 08/108,808
 FILING DATE: 19-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/022,034

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:22:14 ; Search time .796 Seconds
(without alignments)
207.773 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactttggagaaaggct 20

Scoring table: IDENTITY_NUC
GapOp 10_0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 10535742

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

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 Published Applications_NA_Main.*
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 10: /cggn2_6/ptodata/1/pubnra/US11_PUBCOMB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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c 2	20	100.0	29	9 US-10-773-678-158	Sequence 158, APP
c 3	19	95.0	20	9 US-10-773-678-179	Sequence 179, APP
c 4	19	95.0	20	9 US-10-773-678-341	Sequence 341, APP
c 5	18	90.0	20	9 US-10-773-678-343	Sequence 343, APP
c 6	17	85.0	20	9 US-10-773-678-340	Sequence 340, APP
c 7	17	85.0	20	9 US-10-773-678-344	Sequence 344, APP
c 8	16.4	82.0	25	9 US-10-956-15-716-17	Sequence 186717,
c 9	16	80.0	20	9 US-10-957-715-201	Sequence 201, APP
c 10	15.2	76.0	25	9 US-10-956-157-301412	Sequence 301412,
c 11	15.2	76.0	25	10 US-10-956-156-287536	Sequence 287536,
c 12	15	75.0	20	9 US-10-773-678-339	Sequence 339, APP
c 13	15	75.0	20	9 US-10-773-678-345	Sequence 345, APP
c 14	14.8	74.0	25	7 US-10-719-956-13575	Sequence 13575,
c 15	14.8	74.0	25	7 US-10-719-956-196148	Sequence 196148,
c 16	14.8	74.0	25	8 US-10-719-900-181405	Sequence 181405,
c 17	14.8	74.0	25	9 US-10-957-189-124305	Sequence 124305,
c 18	14.8	74.0	25	9 US-10-956-157-205933	Sequence 205933,
c 19	14.4	72.0	25	8 US-10-719-900-611442	Sequence 611442,
c 20	14.4	72.0	25	9 US-10-956-157-178444	Sequence 178444,
c 21	14.4	72.0	25	10 US-11-036-317-95537	Sequence 95537, A
c 22	14.2	71.0	21	8 US-10-751-726-54782	Sequence 54782, A
c 23	14.2	71.0	25	7 US-10-719-956-51664	Sequence 51664, A

ALIGNMENTS

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FILE REFERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 10/713,139
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 09/758,881
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 09/288,461
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 402
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 158
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Probe
US-10-773-678-158

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Query Match 100.0%; Score 20; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 26 GACTCTTGAGGAACGGCT 7

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RESULT 3
Sequence 179, Application US/10773678
Publication No. US20050074879A1
GENERAL INFORMATION:
APPLICANT: Karras, James G
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 10/713,139
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 09/758,881
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 402
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 179
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-179

```

```

Query Match 100.0%; Score 20; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Db 26 GACTCTTGAGGAACGGCT 7

```

Qy 1 GACTCTTGAGGAACGGCT 20
Db 26 GACTCTTGAGGAACGGCT 7

```

RESULT 5
US-10-773-678-343
Sequence 343, Application US/10773678
Publication No. US20050074879A1
GENERAL INFORMATION:
APPLICANT: Karras, James G
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 10/713,139
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 09/758,881
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 402
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 343
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-343

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Qy 2 ACTCTTGAGGAACGGCT 20
Db 1 ACTCTTGAGGAACGGCT 19

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RESULT 4
US-10-773-678-341
Sequence 341, Application US/10773678
Publication No. US20050074879A1
GENERAL INFORMATION:

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RESULT 6
US-10-773-678-340

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```
; Sequence 340, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
; US-10-773-678-340

Query Match 85.0%; Score 17; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 93;
March 17. Conservative 0. Mismatch 0. Indels 0. Gaps 0.
```

RESULT 7
 US-10-73-678-344
 Sequence 344, Application US/10773678
 Publication No. US20050074879A1
 GENERAL INFORMATION:
 APPLICANT: Karras, James G
 TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
 TITLE OF INVENTION: Expression
 FILE REFERENCE: ISPH-0828
 CURRENT APPLICATION NUMBER: US/10/773,678
 CURRENT FILING DATE: 2004-02-06
 PRIOR APPLICATION NUMBER: 10/713,139
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 09/758,881
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: PCT/US00/09054
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: 09/288,461
 PRIOR FILING DATE: 1999-04-08
 NUMBER OF SEQ ID NO: 402
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 344
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense oligonucleotide

```

Query Match Similarity : 85.0%; Score 17; DB 9; Length 20;
Best Local Similarity : 100.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 0; Indels 0;
1 GACTCTTGAGGAAAGCG 17
2 GACTCTTGAGGAAAGCG 17
3 GACTCTTGAGGAAAGCG 17
4 GACTCTTGAGGAAAGCG 20

```

```

RESULT 8
US-10-956-157-186717/c
; Sequence 186717, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 186717
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-186717

Query Match          Score 16.4; DB 9; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GACTCTTGAGGAAAGCGG 18
        ||||| ||||| ||||| |
Db      20 GACTCTTGAGGAAAGCGG 3

RESULT 9
US-10-857-715-201
; Sequence 201, Application US/10857715
; Publication No. US20050164218A1
; GENERAL INFORMATION:
; APPLICANT: Agus David
; APPLICANT: Baker Joffre
; APPLICANT: Natale Ron
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Gene Expression Markers for Response to EGFR Inhibitors Drugs
; FILE REFERENCE: 39740/0011
; CURRENT APPLICATION NUMBER: US/10/857,715
; CURRENT FILING DATE: 2004-05-28
; PRIORITY: 60/4474, 908
; PRIOR APPLICATION NUMBER: 2003-05-30
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 201
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: reverse primer
US-10-857-715-201

Query Match          Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CTTGGCAGGAAGCGGCT 20
        ||||| ||||| ||||| |
Db      1 CTTGCAGGAAGCGGCT 16

RESULT 10
US-10-956-157-301412/c
; Sequence 301412, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
 ; FILE REFERENCE: 031896-041000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US10/956,157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 301412
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Probe Sequence
 ; US-10-956-157-301412

Query Match 76.0%; Score 15.2; DB 9; Length 25;
 Best Local Similarity 85.0%; Pred. No. 8.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGGGCT 20
 Db 23 GCCTTTCGAGGAACGGCT 4

RESULT 11
 US-10-060-756-287536/c
 ; Sequence 287536, Application US/110606756
 ; Publication No. US20050221354A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Dr g
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SEQ ID NO: 287536
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 ; US-11-060-756-287536

Query Match 76.0%; Score 15.2; DB 10; Length 25;
 Best Local Similarity 85.0%; Pred. No. 8.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGGGCT 20
 Db 23 GCCTTTCGAGGAACGGCT 4

RESULT 12
 US-10-773-678-339
 ; Sequence 339, Application US/10773678
 ; Publication No. US20050074879A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Karras, James G
 ; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
 ; FILE REFERENCE: ISPH-0828
 ; CURRENT APPLICATION NUMBER: US/10/773,678
 ; CURRENT FILING DATE: 2004-02-06
 ; PRIOR APPLICATION NUMBER: 10/113,139
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 09/758,881
 ; CURRENT APPLICATION NUMBER: PCT/US00/09054
 ; CURRENT FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 09/288,461
 ; PRIOR FILING DATE: 1999-04-08
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 345
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense oligonucleotide

Query Match 75.0%; Score 15.; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTTTGAGGAG 15
 Db 6 GACTTTGAGGAG 20

RESULT 14
 US-10-719-956-135575/c
 ; Sequence 135575, Application US/10719956
 ; Publication No. US20040146910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527_1
 ; CURRENT APPLICATION NUMBER: US/10/719,956
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,836
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 639466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 135575
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-10-719-956-135575

```

Query Match    74.0%;  Score 14.8;  DB 7;  Length 25;
Best Local Similarity 88.9%;  Pred. No. 1.3e+03;  Matches 16;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;                                ; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/889,189
; PRIORITY NUMBER: 2004-03-25
; PRIOR FILING DATE: 1999-05-15
; PRIOR FILING NUMBER: 60/100,678
; PRIORITY NUMBER: 60/100,678
; PRIORITY FILING DATE: 1998-05-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSNQ for Windows Version 4.0
; SEQ ID NO: 124305
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-124305

Query Match    74.0%;  Score 14.8;  DB 9;  Length 25;
Best Local Similarity 88.9%;  Pred. No. 1.3e+03;  Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;                                ; APPLICANT: Mounts William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319005
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 205933
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-205933

Query Match    74.0%;  Score 14.8;  DB 9;  Length 25;
Best Local Similarity 88.9%;  Pred. No. 1.3e+03;  Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;                                ; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319005
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 205933
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-205933

Query Match    74.0%;  Score 14.8;  DB 7;  Length 25;
Best Local Similarity 88.9%;  Pred. No. 1.3e+03;  Matches 16;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;                                ; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIORITY NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 181405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-181405

Query Match    74.0%;  Score 14.8;  DB 8;  Length 25;
Best Local Similarity 88.9%;  Pred. No. 1.3e+03;  Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;                                ; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIORITY NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 611442
; LENGTH: 25

Query Match    74.0%;  Score 14.8;  DB 7;  Length 25;
Best Local Similarity 88.9%;  Pred. No. 1.3e+03;  Matches 16;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;                                ; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-05-11
; PRIORITY NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSNQ for Windows Version 4.0
; SEQ ID NO: 611442
; LENGTH: 25

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;
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-611442

Query Match    72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; SEQ ID NO: US20050214823A1
Qy      5 CTTGAGGAAGGGCT 20
Db      19 CTTGAGGAAGGGCT 4

RESULT 20
US-10-956-157-178444/C
; Sequence 178444, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-041000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 178444
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-178444

Query Match    72.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; SEQ ID NO: US20050214823A1
Qy      5 CTTGAGGAAGGGCT 20
Db      21 CTTCAGGAAGGGCT 6

RESULT 21
US-10-036-317-955317/C
; Sequence 955317, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 955317
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-955317

Query Match    72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; SEQ ID NO: US20050214823A1
Qy      4 TCTGAGGAAGGGCT 19
Db      20 TCTGAGGAAGGGCT 5

RESULT 22
US-10-809-119-56325
; Sequence 65325, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 2101.1
; CURRENT APPLICATION NUMBER: US/10/809,189

Query Match    71.0%; Score 14.2; DB 8; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.7e+03; Mismatches 3; Indels 0; Gaps 0;
NUMBER OF SEQ ID NOS: 54873
Qy      2 ACTCTTCAGGAAGGGCT 20
Db      21 AATCTCTAGGAAGGGCT 3

RESULT 23
US-10-719-956-51664/C
; Sequence 51664, Application US/10719956
; Publication No. US2004146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 51664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-51664

Query Match    71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03; Mismatches 3; Indels 0; Gaps 0;
NUMBER OF SEQ ID NOS: 51664
Qy      2 ACTCTTCAGGAAGGGCT 20
Db      20 ACTCTTACAGGAGGCCACT 2

RESULT 24
US-10-809-119-56325
; Sequence 65325, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 2101.1
; CURRENT APPLICATION NUMBER: US/10/809,189

Query Match    71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03; Mismatches 3; Indels 0; Gaps 0;
NUMBER OF SEQ ID NOS: 51664
Qy      2 ACTCTTCAGGAAGGGCT 20
Db      20 ACTCTTACAGGAGGCCACT 2

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; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1993-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO: FastSEQ for Windows Version 4.0
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-18-65325

Query Match 71.0%; Score 14.2%; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAACGGC 19
Db 3 GACCCCTGAGGAATGGC 21

RESULT 27
US-11-036-317-255809
; Sequence 255809, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 255809
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-255809

Query Match 71.0%; Score 14.2%; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAACGGC 19
Db 2 GACCCCTGAGGAATGGC 20

RESULT 25
US-11-036-317-193968
; Sequence 193968, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 193968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-193968

Query Match 71.0%; Score 14.2%; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAACGGC 19
Db 5 GACCCCTGAGGAATGGC 23

RESULT 26
US-11-036-317-247028
; Sequence 247028, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 247028
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-247028

Query Match 71.0%; Score 14.2%; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAACGGC 19
Db 1 GACCCCTGAGGAATGGC 19

RESULT 29
US-11-036-317-308860
; Sequence 308860, Application US/11036317
; Publication No. US20050214823A1

```

GENERAL INFORMATION:
i APPLICANT: Blume, John
i TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
i FILE REFERENCE: 3654_1
i CURRENT APPLICATION NUMBER: US/11/036,317
i CURRENT FILING DATE: 2005-01-13
i PRIOR APPLICATION NUMBER: US 60/536,639
i PRIOR FILING DATE: 2004-01-13
i NUMBER OF SEQ ID NOS: 991174
i SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
i SEQ ID NO: 308860
i LENGTH: 25
i TYPE: DNA
i ORGANISM: Mus musculus
US-11-036-317-308860

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGC 19
Db 6 GACTCTTGAGGAATAAGC 24

RESULT 32
US-11-036-317-482672
i Sequence 482672, Application US/11036317
i Publication No. US20050214823A1
i GENERAL INFORMATION:
i APPLICANT: Williams, Alan
i APPLICANT: Blume, John
i TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
i FILE REFERENCE: 3654_1
i CURRENT APPLICATION NUMBER: US/11/036,317
i CURRENT FILING DATE: 2005-01-13
i PRIOR APPLICATION NUMBER: US 60/536,639
i PRIOR FILING DATE: 2004-01-13
i NUMBER OF SEQ ID NOS: 991174
i SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
i SEQ ID NO: 482672
i LENGTH: 25
i TYPE: DNA
i ORGANISM: Mus musculus
US-11-036-317-482672

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGC 19
Db 2 GATTATGGCATGAGCGGC 20

RESULT 33
US-11-036-317-538007
i Sequence 538007, Application US/11036317
i Publication No. US20050214823A1
i GENERAL INFORMATION:
i APPLICANT: Williams, Alan
i APPLICANT: Blume, John
i TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
i FILE REFERENCE: 3654_1
i CURRENT APPLICATION NUMBER: US/11/036,317
i CURRENT FILING DATE: 2005-01-13
i PRIOR APPLICATION NUMBER: US 60/536,639
i PRIOR FILING DATE: 2004-01-13
i NUMBER OF SEQ ID NOS: 991174
i SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
i SEQ ID NO: 4335916
i LENGTH: 25
i TYPE: DNA
i ORGANISM: Mus musculus
US-11-036-317-4335916

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGC 19
Db 1 GACTCTTGAGGAATAAGC 19

RESULT 31
US-11-036-317-473142
i Sequence 473142, Application US/11036317
i Publication No. US20050214823A1
i GENERAL INFORMATION:
i APPLICANT: Williams, Alan
i APPLICANT: Blume, John
i TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
i FILE REFERENCE: 654_1
i CURRENT APPLICATION NUMBER: US/11/036,317
i CURRENT FILING DATE: 2005-01-13
i PRIOR APPLICATION NUMBER: US 60/536,639
i PRIOR FILING DATE: 2004-01-13
i NUMBER OF SEQ ID NOS: 991174
i SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
i SEQ ID NO: 473142
i LENGTH: 25
i TYPE: DNA
i ORGANISM: Mus musculus
US-11-036-317-538007

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGAGGAAGCGGC 19
Db 6 GACTCTGCAAGAGAGGC 24

RESULT 34
; Sequence 63453, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US 11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 634153
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-634153

Query Match 71.0% ; Score 14.2 ; DB 10 ; Length 25 ;
 Best Local Similarity 84.2% ; Pred. No. 2.7e+03 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

Qy 1 GACTCTTGAGGAAGGGC 19
 Db 6 GACTCTTGAGGAATAAGC 24

RESULT 35
; Sequence 648448, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US 11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 648448
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-648448

Query Match 71.0% ; Score 14.2 ; DB 10 ; Length 25 ;
 Best Local Similarity 84.2% ; Pred. No. 2.7e+03 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

Qy 1 GACTCTTGAGGAAGGGC 19
 Db 2 ATTCCTGAGGCAGCGCGCT 3

RESULT 36
; Sequence 773627, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US 11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13

Query Match 71.0% ; Score 14.2 ; DB 10 ; Length 25 ;
 Best Local Similarity 84.2% ; Pred. No. 2.7e+03 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

Qy 1 GACTCTTGAGGAAGGGC 19
 Db 6 GACTCTTGAGGAATAAGC 24

RESULT 37
; Sequence 940292, Application US/11036317
; Publication No. US2005021423A1
; GENERAL INFORMATION:
; APPLICANT: Blume, Alan
; TITLE OF INVENTION: Method of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 940292

Query Match 71.0% ; Score 14.2 ; DB 10 ; Length 25 ;
 Best Local Similarity 84.2% ; Pred. No. 2.7e+03 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

Qy 1 GACTCTTGAGGAAGGGC 19
 Db 6 GACTCTTGAGGAATAAGC 24

RESULT 38
; Sequence 975516, Application US/11036317
; Publication No. US2005021423A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 975516

Query Match 71.0% ; Score 14.2 ; DB 10 ; Length 25 ;
 Best Local Similarity 84.2% ; Pred. No. 2.7e+03 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

Qy 1 GACTCTTGAGGAAGGGC 19

Db 2 GACTACTGAGCGAGGGC 20

RESULT 39
US-09-758-881-19
Sequence 19, Application US/09758881
Patent No. US20010029250A1

GENERAL INFORMATION:

APPLICANT: Karras, James G

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

FILE REFERENCE: ISPH-0532

CURRENT APPLICATION NUMBER: US/09/758,881

CURRENT FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 09/288,461

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 152

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19

Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCTTTGAGGAA 14

DB 7 GACTCTTGCAGGAA 20

RESULT 40
US-10-773-678-19

Sequence 19, Application US/10773678
Publication No. US20050074879A1

GENERAL INFORMATION:

APPLICANT: Karras, James G

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

FILE REFERENCE: ISPH-0828

CURRENT APPLICATION NUMBER: US/10/773,678

CURRENT FILING DATE: 2004-02-06

PRIOR APPLICATION NUMBER: 10/713,139

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 09/758,881

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 09/288,461

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 402

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-773-678-19

Query Match 70.0%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACCTTTGAGGAA 14

November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid databases now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for them daily updates. This results in more machine time being available for processing searches. Newly published applications will appear in the Published Applications Main databases, older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions .runpbm (Published Applications AA Main) and .rappbm (Published Applications AA New). Searches run against Amino Acid Published Applications produce two sets of results, with the extensions .runpbm (Published Applications NA Main) and .rappbm (Published Applications NA New).

Searches run against Published Applications produce two sets of results, with the extensions .rappbm (Published Applications AA Main) and .rappbm (Published Applications AA New).

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:30:06 ; Search time 233 Seconds
(without alignments)
26.714 Million cell updates/sec

Title: US-10-773-678A-342
Perfect score: 20
Sequence: 1 gactctcgaggaaaggcggt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6442102

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

RESULT 1
US-11-102-228-233
 Published Applications_NA_New:
 1: /cgn2_6/podata/1/pubnra/us09 NEW PUB.seq:
 2: /cgn2_6/podata/1/pubnra/us06 NEW PUB.seq:
 3: /cgn2_6/podata/1/pubnra/us07 NEW PUB.seq:
 4: /cgn2_6/podata/1/pubnra/us01 NEW PUB.seq:
 5: /cgn2_6/podata/1/pubnra/pct NEW PUB.seq:
 6: /cgn2_6/podata/1/pubnra/us10 NEW PUB.seq:
 7: /cgn2_6/podata/1/pubnra/us03 NEW PUB.seq:
 8: /cgn2_6/podata/1/pubnra/us11 NEW PUB.seq:
 9: /cgn2_6/podata/1/pubnra/us11_NEW_PUB.seq3:
 10: /cgn2_6/podata/1/pubnra/us60_NEW_PUB.seq:
 *score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	80.0	20	7 US-11-102-228-233	Sequence 233, App
c 2	14.4	72.0	19	8 US-11-101-244-1280351	Sequence 1290351,
c 3	14.4	72.0	19	8 US-11-101-244-1280351	Sequence 1290351,
c 4	13.8	69.0	19	8 US-11-101-244-43270	Sequence 439270,
c 5	13.8	69.0	19	9 US-11-101-244-43270	Sequence 439270,
c 6	13.4	67.0	19	8 US-11-101-244-1280317	Sequence 1290317,
c 7	13.4	67.0	19	9 US-11-101-244-1280317	Sequence 1290317,
c 8	13.2	66.0	19	8 US-11-101-244-55327	Sequence 556327,
c 9	13.2	66.0	19	9 US-11-101-244-55327	Sequence 556327,
c 10	13	65.0	19	8 US-11-101-244-96873	Sequence 968731,
c 11	13	65.0	19	8 US-11-101-244-96873	Sequence 968731,
c 12	13	65.0	19	8 US-11-101-244-1065415	Sequence 1065415,
c 13	13	65.0	19	9 US-11-101-244-1065415	Sequence 968731,
c 14	13	65.0	19	9 US-11-101-244-155594	Sequence 968731,
c 15	13	65.0	19	9 US-11-101-244-155594	Sequence 968731,
c 16	12.8	64.0	19	8 US-11-101-244-1169015	Sequence 1169015,
c 17	12.8	64.0	19	8 US-11-101-244-1169015	Sequence 1169015,
c 18	12.8	64.0	19	8 US-11-101-244-1552463	Sequence 1552463,
c 19	12.8	64.0	19	8 US-11-101-244-155594	Sequence 155594,
c 20	12.8	64.0	19	9 US-11-101-244-155594	Sequence 155594,
c 21	12.8	64.0	19	9 US-11-101-244-155594	Sequence 155594,
c 22	12.8	64.0	19	9 US-11-101-244-155594	Sequence 155594,
c 23	12.8	64.0	19	9 US-11-101-244-155594	Sequence 155594,

RESULT 2
US-11-101-244-1290351/c
 General Information: Dharmacon, Inc.
 Sequence 1290351, Application US/11101244
 Publication No. US20050246794A1
 Applicant: Khorrova, Anastasia
 Applicant: Reynolds, Angela
 Applicant: Leake, Devin
 Applicant: Marshall, William
 Applicant: Scarling, Stephen
 Title of Invention: Functional and Hyperfunctional siRNA
 File Reference: 13499015
 Current Application Number: US/11/101,244

ALIGNMENTS

CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIORITY FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIORITY FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1290351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1290351

Query Match 72.0%; Score 14.4; DB 8; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 TCTTGAGGAAGGGC 19
Db 16 TCTTGAGGAAGGC 1

RESULT 4

US-11-083-784-1290351/c
; Sequence 1290351, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1290351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1290351

Query Match 72.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGAGGAAGGGC 19

Db 16 TCTTGAGGAAGGC 1

RESULT 4

US-11-101-244-439270/c
; Sequence 439270, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Pharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 439270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-439270

Query Match 69.0%; Score 13.8; DB 8; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e+02; Indels 2; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ACTCTGCGAGAACGG 18
Db 17 ACTCTGCGGAGACGG 1

RESULT 5

US-11-083-784-439270/c
; Sequence 439270, Application US/11083784
; Publication No. US2005024475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 439270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-439270

Qy 2 ACTCTGCGAGAACGG 18

Db 17 ACTCTGCGGAGACGG 1

RESULT 6

US-11-101-244-1290317/c
; Sequence 1290317, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIORITY NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIORITY NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 1290317
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-1290317

Query Match 67.0%; Score 13.4; DB 9; Length 19;
 Best Local Similarity 93.3%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Insertions 1; Deletions 0;
 Qy 6 TTGCAGGAAGGGCT 20
 Db 19 TTGCAGGAAGGAGCT 5

RESULT 7
 US-11-083-784-1290317/c
 ; Sequence 1290317, Application US/11083784
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIORITY NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIORITY NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIORITY NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 1290317
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1290317

Query Match 67.0%; Score 13.4; DB 9; Length 19;
 Best Local Similarity 93.3%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 1; Mismatches 1; Insertions 1; Deletions 0;
 Qy 6 TTGCAGGAAGGGCT 20
 Db 19 TTGCAGGAAGGAGCT 5

RESULT 8
 US-11-101-244-556327/c
 ; Sequence 556327, Application US/11101244
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11101244
 CURRENT FILING DATE: 2005-04-07
 PRIORITY NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIORITY NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIORITY NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 556327
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-556327

RESULT 9
 US-11-083-784-556327/c
 ; Sequence 556327, Application US/11083784
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11101244
 CURRENT FILING DATE: 2005-04-07
 PRIORITY NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIORITY NUMBER: 60/502,050
 PRIOR FILING DATE: 2002-11-14
 PRIORITY NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 556327
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-556327

Query Match 66.0%; Score 13.2; DB 8; Length 19;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Insertions 3; Deletions 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCGC 19
 Db 18 ACTCTTCCAGGCCAGTCGC 1

Query Match 66.0%; Score 13.2; DB 8; Length 19;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Insertions 3; Deletions 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCGC 19
 Db 18 ACTCTTCCAGGCCAGTCGC 1

Query Match 66.0%; Score 13.2; DB 8; Length 19;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Insertions 3; Deletions 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCGC 19
 Db 18 ACTCTTCCAGGCCAGTCGC 1

Query Match 66.0%; Score 13.2; DB 8; Length 19;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Insertions 3; Deletions 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGGGCGC 19
 Db 18 ACTCTTCCAGGCCAGTCGC 1

APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIORITY NUMBER: 60/502,050
 PRIOR APPLICATION NUMBER: 2003-09-10
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 968803
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-968803

Query Match 65.0%; Score 13; DB 8; Length 19;
 Best Local Similarity 76.9%; Pred. No. 6.7e+02;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAAGGAGC 16
 Db 3 UCUGCAGGAAGC 15

RESULT 11
 US-11-101-244-968803
 Sequence 968803, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khorrova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIORITY NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 968803
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-968803

Query Match 65.0%; Score 13; DB 8; Length 19;
 Best Local Similarity 76.9%; Pred. No. 6.7e+02;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAAGGAGC 16
 Db 3 UCUGCAGGAAGC 15

RESULT 12
 US-11-101-244-1066415
 Sequence 1066415, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khorrova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen

Query Match 65.0%; Score 13; DB 9; Length 19;
 Best Local Similarity 76.9%; Pred. No. 6.7e+02;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAAGGAGC 16
 Db 3 UCUGCAGGAAGC 15

RESULT 13
 US-11-083-784-968731
 Sequence 968731, Application US/11083784
 Publication No. US20050245475A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khorrova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIORITY NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 968731
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-968731

Query Match 65.0%; Score 13; DB 9; Length 19;
 Best Local Similarity 76.9%; Pred. No. 6.7e+02;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAAGGAGC 16
 Db 3 UCUGCAGGAAGC 15

APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 968803
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-968803

Query Match 65.0%; Score 13; DB 9; Length 19;
 Best Local Similarity 76.0%; Pred. No. 6.7e+02; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGAGGAAGC 16
 : :: ||| | | | |
 Db 3 UCUUGCAAGGAAGC 15

RESULT 15
 US-11-083-784-1066415
 / Sequence 106615, Application US/11083784
 / Publication No. US20050245475A1
 / GENERAL INFORMATION:
 / APPLICANT: Dharmacon, Inc.
 / APPLICANT: Khorrova, Anastasia
 / APPLICANT: Reynolds, Angela
 / APPLICANT: Leake, Devin
 / APPLICANT: Marshall, William
 / APPLICANT: Scaringe, Stephen
 / TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 / FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 1066415
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1066415

Query Match 65.0%; Score 13; DB 9; Length 19;
 Best Local Similarity 92.3%; Pred. No. 6.7e+02; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCAGGAGCGGACT 20
 : | | | | | | | | | |
 Db 1 GCAGGAGCGGCU 13

RESULT 16
 US-11-101-244-21319/C
 / Sequence 21319, Application US/11101244
 / Publication No. US20050246794A1
 / GENERAL INFORMATION:
 / APPLICANT: Dharmacon, Inc.
 / APPLICANT: Khorrova, Anastasia
 / APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 21319
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-21319

Query Match 64.0%; Score 12.8; DB 8; Length 19;
 Best Local Similarity 87.5%; Pred. No. 8.5e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTCAGGAAGCGGC 19
 : | | | | | | | | | |
 Db 17 TCTGAAGGGAGTGC 2

RESULT 17
 US-11-101-244-1169015/C
 / Sequence 1169015, Application US/11101244
 / Publication No. US20050246794A1
 / GENERAL INFORMATION:
 / APPLICANT: Dharmacon, Inc.
 / APPLICANT: Khorrova, Anastasia
 / APPLICANT: Reynolds, Angela
 / APPLICANT: Leake, Devin
 / APPLICANT: Marshall, William
 / APPLICANT: Scaringe, Stephen
 / TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 / FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 1169015
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-1169015

Query Match 64.0%; Score 12.8; DB 8; Length 19;
 Best Local Similarity 87.5%; Pred. No. 8.5e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTGGAGGAAC 16
 : | | | | | | | | | |
 Db 19 GAATCTGGAGGAAC 4

RESULT 18
 US-11-101-244-1552463/C
 / Sequence 1552463, Application US/11101244
 / Publication No. US20050246794A1
 / GENERAL INFORMATION:
 / APPLICANT: Dharmacon, Inc.
 / APPLICANT: Khorrova, Anastasia
 / APPLICANT: Reynolds, Angela

RESULT 19
US-11-101-244-1585494/C
Sequence 1585494, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Dharmaccon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1585494
LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1585494

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ACTCTTGAGGAAGCG 17
Db 19 ACTATGAGGATGCG 4

RESULT 19
US-11-101-244-1585494/C
Sequence 1585494, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Dharmaccon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1585494
LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1585494

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GACTCTTGAGGAAGC 16
Db 19 GAATCTGGAGGAGC 4

RESULT 20
US-11-083-784-21319/C
Sequence 21319, Application US/11083784
; GENERAL INFORMATION:
; APPLICANT: Dharmaccon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1169015
LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-21319

RESULT 21
US-11-083-784-11169015/C
Sequence 11169015, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaccon, Inc.
; APPLICANT: Khrorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1169015
LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-11169015

RESULT 22
US-11-083-784-1552463/C
Sequence 1552463, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaccon, Inc.

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCTTGAGGAAGCGC 19
Db 17 TCTGAAGGAAGTGC 2

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCTTGAGGAAGCGC 19
Db 17 TCTGAAGGAAGTGC 2

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GACTCTTGAGGAAGC 16
Db 19 GAATCTGGAGGAGC 4

APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scarine, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 134990US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 1552463
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1552463

Query Match 64.0%; Score 12.8; DB 9; Length 19;
 Best Local Similarity 87.5%; Pred. No. 8.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;
 Qy 2 ACTCTTGAGGAGGCG 17
 Db 19 ACTCATGGATGCG 4

RESULT 23

US-11-083-784-1585494/C

Sequence 1585494, Application US/11083784
 Publication No. US20050245475A1
 GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin

APPLICANT: Marshall, William
 APPLICANT: Scarine, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 134990US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO: 1585494
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1585494

Query Match 64.0%; Score 12.8; DB 9; Length 19;
 Best Local Similarity 87.5%; Pred. No. 8.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;
 Qy 1 GACTCTTGAGGAGC 16
 Db 19 GAATCTGGAGGAAGC 4

RESULT 24

US-11-090-739-13/c

Sequence 13, Application US/11090739
 Publication No. US20050260639A1
 GENERAL INFORMATION:

APPLICANT: NAKAMURA, Yusuke
 APPLICANT: KATAGIRI, Toyosawa
 APPLICANT: NAKAGAWA, Hidemaki

TITLE OF INVENTION: METHOD FOR DIAGNOSING PANCREATIC CANCER

FILE REFERENCE: 082368-001600US

CURRENT APPLICATION NUMBER: US/11/090,739

CURRENT FILING DATE: 2005-03-24

PRIOR APPLICATION NUMBER: PCT/JP2003/011817

PRIOR FILING DATE: 2003-05-17

PRIOR APPLICATION NUMBER: US 60/555,809

PRIOR FILING DATE: 2004-03-24

PRIOR APPLICATION NUMBER: US 60/450,889

PRIOR FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: US 60/414,872

PRIOR FILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 153

SOFTWARE: PatentIn version 3.3

SEQ ID NO: 13

LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial

OTHER INFORMATION: Artificially synthesized primer sequence for RT-PCR

US-11-090-739-13

Query Match 63.0%; Score 12.6; DB 7; Length 20;
 Best Local Similarity 78.9%; Pred. No. 1.1e-03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0;
 Gaps 0;

Qy 2 ACTCTTGAGGAGGGCT 20

Db 20 AATCTCCAGGAAGGTGCT 2

RESULT 24
 US-10-750-185-14564
 Sequence 14564, Application US/10750185

RESULT 26
US-11-101-244-251435/c
; Sequence 251435, Application US/11101244
; Publication No. US20050246794A1
GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIORITY APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 251435
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-251435

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 ACTCTTGAGGAAG 15
Db 1B ACTCTTGAGGTAG 5

** RESULT 27
US-11-101-244-251481/c
; Sequence 251481, Application US/11101244
; Publication No. US20050246794A1
GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIORITY APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 251481
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-251481

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 ACTCTTGAGGAAG 15
Db 1B ACTCTTGAGGTAG 4

RESULT 28
US-11-101-244-1337482/c
; Sequence 1337482, Application US/11101244
; Publication No. US20050246794A1
GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIORITY APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 1337482
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1337482

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 ACTCTTGAGGAAG 15
Db 1B ACTCTTGAGGTAG 5

RESULT 29
US-11-083-784-251435/c
; Sequence 251435, Application US/11083784
; Publication No. US2005024575A1
GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIORITY APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIORITY APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 251435
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-251435

Query Match 62.0%; Score 12.4; DB 9; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 ACTCTTGAGGAAG 15
Db 1B ACTCTTGAGGTAG 5

RESULT 30
US-11-083-784-251481/c
; Sequence 251481, Application US/11083784
; GENERAL INFORMATION
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, Stephen
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 251481
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-251481

Db 18 ACTCTTGAGAAAG 5

RESULT 32
US-11-101-244-186562/c
; Sequence 186562, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 186562
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-186562

Query Match 62.0%; Score 12.4; DB 9; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 1; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAG 15
Db 17 ACTCTTGAGGTAG 4

RESULT 31
US-11-083-784-1337482/c
; Sequence 1337482, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1337482
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1337482

Db 18 ACTCTTGAGAAAG 5

RESULT 33
US-11-101-244-199830/c
; Sequence 199830, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 199830
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-199830

Query Match 62.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGGGCT 20
Db 19 TCATCGAGCAAGTGGCT 3

RESULT 34
US-11-101-244-199830/c
; Sequence 199830, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 199830
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-199830

Query Match 62.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGGGCT 20
Db 19 TCATCGAGCAAGTGGCT 3

RESULT 34 US-11-101-244-266845/c Sequence 266845, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 266845
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-266845
 Query Match 61.0%; Score 12.2; DB 8; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 CTCCTGCAAGAGCGC 19
 Db 17 CCTCTGCAAGTAGCGGC 1
 RESULT 35 US-11-101-244-266905/c Sequence 266905, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 266905
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-266905
 Query Match 61.0%; Score 12.2; DB 8; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 CTCCTGCAAGAGCGC 19
 Db 17 CCTCTGCAAGTAGCGGC 1

RESULT 36 US-11-101-244-277581/c Sequence 277581, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 277581
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-277581
 Query Match 61.0%; Score 12.2; DB 8; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 TCTTGAGGAAGCGGCT 20
 Db 19 TCATTCAGGATGCGGT 3
 RESULT 37 US-11-101-244-487058/c Sequence 487058, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 487058
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-487058
 Query Match 61.0%; Score 12.2; DB 8; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 TCTTGAGGAAGCGGCT 20
 Db 19 TCATTCAGGATGCGGT 3

RESULT 38
 US-11-101-244-726311/c
 ; Sequence 726311, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khorrova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIORITY NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIORITY NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 726311
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-726311

Query Match 61.0%; Score 12.2; DB 8; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Gaps 0;
 Qy 4 TCTTGCAGGAAGGGCT 20
 | | | | | | | | | | | | | | | |
 Db 19 TCTTGCAGGAAGCCGGT 3

Search completed: December 3, 2005, 15:27:10
 Job time : 234 secs

RESULT 39
 US-11-101-244-855529/c
 ; Sequence 855529, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khorrova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIORITY NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIORITY NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO: 855529
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-855529

Query Match 61.0%; Score 12.2; DB 8; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCATCAGGAAGGGC 19
 | | | | | | | | | | | | | | | |
 Db 17 CTGTTCAGGAGTC 1

RESULT 40

Query Match 61.0%; Score 12.2; DB 8; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Gaps 0;
 Qy 4 TCTTGCAGGAAGGGCT 20
 | | | | | | | | | | | | | | | |
 Db 18 TGTGGAGGAAGGGCT 2

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